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UNITED STATES DISTRICT COURT

WESTERN DISTRICT OF WISCONSIN

PROMEGA CORPORATION,

Plaintiff,

MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN E.V.,

Involuntary Plaintiff,

v.

LIFE TECHNOLOGIES CORPORATION, INVITROGEN IP HOLDINGS, INC., and APPLIED BIOSYSTEMS, INC.,

Defendants.

Case No.: 10-CV-281

EXPERT REPORT OF JACK BALLANTYNE

The following information is provided pursuant to Rule 26(a)(2)(B):

1. A complete statement of all opinions to be expressed by me at trial and the basis and reasons for all such opinions is attached hereto as **Attachment 1**. I reserve the right to supplement this report, as appropriate, after reviewing any further information provided in the case.
2. The data and other information considered by me in forming the opinions noted in paragraph one are identified in Attachment 1.
3. A copy of my curriculum vitae, which includes my qualifications and a list of all publications authored by me is attached hereto as Attachment 2.
4. I am a Professor in the Department of Chemistry at the University of Central Florida and an Associate Director of Research at the National Center for Forensic Science, Orlando, Florida.
5. While I have provided testimony in criminal proceedings, I have not provided any testimony in U.S. civil proceedings in the last four years.
6. I am being compensated for this report at a rate of $200/hour.
7. Having been informed that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the U.S. Code, I declare under penalty of perjury that the following is true and correct.

Dated this 11 day of July, 2011.

Jack Ballantyne

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ATTACHMENT 1 TO EXPERT REPORT OF JACK BALLANTYNE

If called to testify in this case, I will express the following opinions at trial, the basis and reasons for which are set forth below and detailed in the documentation identified below. I reserve the right to supplement these opinions in the event of new information

1. In preparing this report, I reviewed the so-called Tautz Patent (RE37,984) as well as the Promega Patents, i.e. U.S. Patent Nos. 5,843,660 (‘660); 6,221,598 (‘598); 6,479,235 (‘235); and 7,008,771 (‘771). I am familiar with the technology utilized in these patents. The Promega Patents disclose and claim methods of simultaneously determining specified DNA markers in a human genome by multiplexing. The primary applications for these methods in the past have been in the fields of forensic analysis, DNA typing, and paternity determination. The nature of each of these fields is briefly discussed below.

A. Nature of the Fields Applicable to STR Multiplexing

2. For the reasons detailed below, it is my opinion that the use of STR multiplex kits in the following applications are not “Forensics” or “Human Identity” or “Paternity” applications: monitoring bone marrow transplant engraftment; genotyping hydatidiform moles, and confirming that cell lines are genetically unique (cell line authentication).
3. A useful definition for Forensic Testing is found on the Human Identity Trade Association (HITA) website (http://humanidentity.org):

"Forensic DNA testing serves a number of useful purposes. It can be used to track down criminal suspects who have left behind biological evidence, exonerate individuals who have been falsely accused of committing crimes, identify individuals who have fallen victim to violent crimes or disasters, and connect crimes that share biological

evidence. It can also be used to identify the father of a child conceived through rape or incest."

To summarize, forensic uses are legal in nature and include a) uses to inculpate perpetrators and exclude falsely accused individuals, b) uses to identify victims of a violent crime or mass fatality, or c) identify the father in a criminal paternity case.

4. Over the years, I have been involved in forensic work associated with criminal cases as well as human identification work of victims of a mass fatality. With regard to the latter, I was the forensic scientist who led the DNA identification effort on TWA Flight 800, which exploded and crashed just after takeoff in 1996, killing everyone on board. The case was particularly challenging since, even as late as nine months after the crash, investigators were still dredging up human remains off the ocean floor.

5. Disaster victim identification until the mid- to late-1990s relied mainly on traditional methods, such as analysis of fingerprints and teeth. DNA testing initially played a relatively minor supporting role either in bolstering other methods or being used as a last resort when all else has failed. See J. Ballantyne, "Mass Disaster Genetics," *Nat. Genet*. 15:329 (1997) (Exhibit 1). However, DNA testing emerged as a primary tool in the late 1990s and early 2000s, with the work on TWA Flight 800 and the 9/11 disaster being examples of this change. L. Biesecker et al., "DNA Identifications after the 9/11 World Trade Center Attack," Science 310:1122 (2005) (Exhibit 2).

6. My own research includes testing with commercial kits, such as the Promega and ABI kits, to develop improved conditions for getting the best results for forensic purposes. See, for example, K. Mayntz-Press and J. Ballantyne, "Performance Characteristics of

Commercial Y-STR multiplex systems," *J. Forensic Sci.* 52:1025 (2007) (attached hereto as Exhibit 3).

7. Forensics involves human identity testing. The fundamental question for human identity testing is: who is this person? The process starts with a sample, the human source of which is unknown, and (if successful) proceeds to the identification of the human from which the sample is derived.

8. [redacted]

9. [redacted]

10. "DNA typing" is a more general term than Forensic or Paternity testing. DNA typing can involve the typing of tissue where the question is <u>not</u>: who is this person? For example, DNA typing by multiplexing STR loci today is routinely done for research purposes and for clinical purposes, e.g. clinical diagnostic and treatment purposes. Clinical diagnostics

involves diagnostics in a clinical setting, e.g. a setting for patient treatment. Similarly, clinical research involves research in a clinical setting. It typically involves the use of human subjects or materials derived from human subjects. By contrast, research that is not done in a clinical setting is typically done in a laboratory, e.g. at a university.

11. Starting in the mid-1990s, there has been a growing use of commercial STR multiplexing kits for clinical purposes, including but not limited to monitoring bone marrow transplantation engraftment, genotyping hydatidiform moles, characterizing and diagnosing cancer, and contamination testing (including cell line authentication). See J. Pfeifer et al., The Changing Spectrum of DNA-based Specimen Provenance Testing in Surgical Pathology, *Am. J. Clin. Path.*, 135:132 (2011).(attached as Exhibit 4). All of these applications of STR multiplexing are distinct from forensic and paternity applications.

12. The monitoring of bone marrow transplants in human patients is done in a clinical setting, i.e. the transplant is done for the treatment of the patient. The fundamental question involved in monitoring transplant engraftment using STR multiplexing is <u>not</u>: who is this person? It is not for the purpose of human identity because, after all, the identity of the donor and recipient in the transplant is known. Rather, it is to get an idea of how the transplant is taking, i.e. whether it is successfully engrafting. Thus, this clinical field is clearly distinct from the forensic field.

13. That clinical uses are distinct from forensic and paternity uses can be seen from the language of the Promega patents. For example, the ‘771 Patent notes that the technology has specific uses “in the field of forensic analysis, paternity determination, monitoring of

bone marrow transplantation, linkage mapping, and detection of genetic diseases and cancers." ('771 Patent, col. 5, lines 50-53).

14. With regard to the field of paternity testing, the HITA website once again has a useful definition for parentage testing, which includes paternity testing:

"Parentage testing is the examination and comparison of an alleged parent's and a child's genetic profiles to determine whether the individuals are biologically related as parent and child. There are two types of parentage tests: paternity tests and maternity tests."

Thus, where one is not seeking to determine the parent of a child by comparing BOTH profiles, it would not fall in the definition.

15. Certainly, monitoring bone marrow engraftment from a transplant between adults would not fall within the above-noted paternity testing definition. Moreover, even where a child and a parent are involved in the bone marrow transplant, the testing would not be "to determine whether the individuals are biologically related."

16. Thus, monitoring bone marrow engraftment using STR multiplexing is outside the field of paternity testing. The patient material is simply being "tissue typed" to ensure the graft has taken hold in the recipient (and to what extent).

17. [redacted]

[redacted]

18. STR multiplexing can be very useful in other clinical situations, such as genotyping hydatidiform moles. See K. Murphy et al., Molecular Genotyping of Hydatidiform Moles, *J. Mol. Diag*. 11:598 (2009) (attached hereto as Exhibit 5). Unfortunately, distinguishing between different types based on morphology is difficult, with groups reporting "poor interobserver and intraobserver reproducibility." See F. Lipata et al., Precise DNA Genotyping Diagnosis of Hydatidiform Mole, Obstetrics & Gynec. 115: 784 (2010) (introduction section) (attached hereto as Exhibit 6). Commercially available ABI STR multiplexing kits have been found to be "applicable to routine practice for classifying molar specimens." See K. Murphy et al., Molecular Genotyping of Hydatidiform Moles, *J. Mol. Diag*. 11:598 at page 604 (2009) (attached hereto as Exhibit 5).

19. The fundamental question involved in classifying molar specimens using STR multiplexing is not: who is this person? It is not for the purpose of human identity because, after all, the identity of the person with molar pregnancy is known. It is also not for the purpose of determining the father. Rather, it is done to determine whether mother is at risk for more serious disease and/or to determine a course of treatment.

20. STR multiplexing is also useful to assist in confirming that cell lines are genetically unique. This is useful in a variety of settings, including clinical research and basic research. In one study, STR multiplexing with commercially available ABI kits was performed on 40 reported thyroid cancer-derived cell lines, only to reveal that a) many were not unique, and b) some were not even of thyroid origin. See R. Schweppe et al.,

Deoxyribonucleic Acid Profiling Analysis of 40 Human Thyroid Cancer Cell Lines Reveals Cross-Contamination Resulting in Cell Line Redundancy and Misidentification, *J. Clin. Endocrinol. Metab*. 93:4331 (2008) (attached hereto as Exhibit 7) (see Abstract). As noted in this report (p. 4332), the NIH now recognizes this problem and requires cell authentication with grant applications.

21. Cell line authentication is yet another type of generic tissue typing. It is not human identity testing because the human source of the cell line is already known and, therefore, not typically sought. Rather, it is a measure of the genetic integrity and genetic uniqueness of the cell line.

22. Cell line authentication is not a problem related to forensic or paternity work. It is not a problem for human identity testing since the fundamental question is not: who is this person? The problem can invalidate a researcher's published data. This is because the cell line is not what the researcher thought it was; indeed, sometimes the cell line is not the correct species or cell type.

23. Screening of cells such as cultured cells to detect cross-contamination is not related to forensic or paternity work. It is also not human identity testing since the fundamental question is not: who is this person? Rather, the question is: have the cells from my known source become contaminated with other cells?

24. Below, I have attempted to assist the court in understanding the STR technology by providing a brief tutorial.

A. Tutorial Regarding the STR Technology At Issue

25. The human genome is comprised of the DNA present in the 23 pairs of chromosomes existing in the nucleus of human cells. This genomic DNA is made of two

complementary "strands" or "sequences" of "nucleotides" or "bases." The nucleotides in DNA are only four in number and are paired in a defined manner. The four nucleotides are adenine (A), thymine (T), guanine (G) and cytosine (C). An (A) is complementary to, and pairs only with (T); a (C) is complementary to, and pairs only with a (G).

26. The combinations of genetic information at multiple locations in genomic DNA are unique to each individual. It is this fact that forms the premise for genetic identity testing. To use DNA to identify an individual, one can target and identify certain locations or "loci" on the chromosomes which are polymorphic within a population, i.e., loci that vary from individual to individual within the population. These loci are useful as identifiers only when they exhibit a high degree of variation within the population, since if they were largely the same from individual to individual within the population, their ability to distinguish any one individual from another would be minimal.

27. The more a specified locus varies within a population, i.e., the more it varies from individual to individual, the more "polymorphic" the locus is said to be. No one locus alone, however, will positively identify an individual to a statistically significant degree, since no one locus is unique to each individual within any given population. Consequently, for purposes of forensic and paternity determinations, the identification of multiple polymorphic loci is necessary. Indeed, the more polymorphic the loci used in the identification process, the more accurate the identification becomes because the statistical probability of a match between the DNA sample and the individual in question increases exponentially as additional matching loci are identified.

28. The goal is to use enough loci with sufficient polymorphic characteristics such that the identification is so statistically significant that the result cannot be reasonably disputed,

i.e., the individual is identified beyond any reasonable doubt. For example, using Promega's genetic identity products, one can identify an individual's DNA with a power of discrimination exceeding 1 in 100,000,000,000. However, where the DNA sample is of poor quality, the power of discrimination can be less than this.

29. STRs are loci found within genomic DNA that have a number of short repetitive nucleotide sequences. Different authors have slightly different definitions with regard to the repeat length that is considered an STR. Nonetheless, a degree of standardization of the definition of repeat length has been achieved by the International Society for Forensic Genetics (ISFG).

30. The DNA sequences at a particular STR locus within a given population will exhibit a variable number of these repeat sequences. For some individuals within a given population the sequence will repeat 7 times, for others 8 times, for others 4 and so on. It is this variation in the number of repeats at a particular locus that is responsible for the polymorphism, which permits scientists to genetically distinguish one individual from another.

31. The particular genetic information or base sequence associated with a segment of DNA at a particular STR locus in one individual, is called an “allele.” The alleles are numbered in accordance with the number of repeated nucleotide motifs (the "motif” is the specific nucleotide sequence, e.g., AATG, of the short tandem repeat).

32. To understand the meaning of the term “co-amplifying” in step (c) of these various independent method Claims of the Promega Patents, it is helpful to understand the commonly known term “amplifying.” The term "amplify" refers to a process in which multiple copies of the alleles present at the STR loci are made. The STR regions of the

DNA must be "amplified" to be visualized or detected because they are present in too low a concentration to be detected among the rest of the human DNA.

33. PCR is one method of amplifying. There are several steps in the PCR process. First, the "double stranded" or two strands of genomic DNA are separated or "denatured," thereby forming "single stranded" DNA. This denaturation step is done by heating the DNA to a certain temperature, which is sufficient to cause the two strands to separate. Second, a pair of PCR "primers" is introduced and allowed to hybridize or pair with the single stranded DNA. "Hybridization" occurs when the PCR primers "anneal" or join to a single strand of the DNA.

34. The temperature at which the primers anneal to the DNA is one of the variables when developing a multiplex (see paragraph 40, below, for a discussion of multiplexing). That is to say, it is a condition of the amplification reaction that can be changed in an attempt to get a multiplex to work. However, there are limits to such changes. For example, Figure 4-2 of the User's Manual for the ABI Identifiler® PCR Amplification Kit (Exhibit 13) shows the impact of the annealing temperature on product generation. As one increases the temperature, one can reduce the yield of amplified product. *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems* [see lower panels].

35. This hybridization occurs in accordance with the nucleotide pairing rules (e.g. A with T, etc.) noted above, i.e., at a point on the single stranded DNA where the PCR primer sequence is complementary to the genomic nucleotide sequence. Referring to the two opposing primers as the "forward" or "reverse" PCR primer differentiates each primer in the pair.

36. There is a definition of "primers" or "primer" in the specifications of all of the Promega Patents and these definitions are consistent with how the term is understood to one skilled in the art.

37. The PCR primers hybridize at points on the genomic DNA that are adjacent to, or "flank," the actual STR locus. These "flanking regions" are used as the point of hybridization because they are not polymorphic, i.e., they contain the same sequence of nucleotides for all individuals within a given population even though the number of repeats contained in the STR locus between the flanking regions varies from individual to individual. This ensures that all alleles in all individuals will be amplified.

38. The third step of the PCR process is extension of the primers that have hybridized to the single stranded DNA molecules to convert them into double stranded molecules. An enzyme known as a "DNA polymerase" accomplishes this extension process. The polymerase reads the sequence of the single stranded DNA beginning at the primer location and attaches the complementary nucleotides to the primer guided by the opposite strand (As to Ts and Cs to Gs), thereby making it double stranded. These three steps are then repeated many times to amplify the locus of interest.

39. Amplifying the alleles present at a single STR locus is commonly referred to as a "monoplex" reaction. If one wanted to use eight STR loci in an analysis of a particular sample, one could carry out eight separate monoplex reactions amplifying eight separate STR loci. Monoplexing was the initial method employed when using STR loci for DNA analysis.

40. Multiplexing is key to realizing the advantages of STRs for determining genetic identity. Often, one must be able to simultaneously amplify and analyze multiple STRs from a

relatively small amount of sample. That could only be accomplished if it were possible to multiplex the amplification of STR alleles in such a way that you could still determine all of the alleles present at each locus. The Promega Patents accomplished that result.

41. In order to determine the amplified alleles that are present, they are typically segregated from the amplification (e.g. PCR) reaction mixture or otherwise individually detected. One such process used to separate the alleles is known as "electrophoresis." Polyacrylamide gel electrophoresis (PAGE) is one type of electrophoresis that can be used. Capillary gel electrophoresis (CE) is another type of electrophoresis that can be used.

42. While the term "gel" is used in the various patents of this case, the nature of the gel need not be (and often is not) the same for each technique. Agarose gels used to separate DNA are not crosslinked and typically comprise between 1 and 3% agarose, which is a linear polymer made up of disaccharide (sugar) units. Polyacrylamide gels used in slab gels (discussed more below) are typically crosslinked.

43. Uncrosslinked polyacrylamide (or a derivative thereof) is frequently used in CE. While one might be tempted not to call this material a "gel" because it may not be semi-solid, a number of people in the field refer to this material as a gel. For example, the authors of Chapter 16 of Landers et al. refers to such materials as gels: "The development of replaceable non-crosslinked or linear polyacrylamide gels for DNA sequencing was probably the most significant advance made in the field of CE during the 1990s. In replaceable gels, a dynamic network of entangled linear polymers forms the pores through which the DNA is sieved." See Chapter 16: "DNA Sequencing by Capilllary Electrophoresis," by David Yang et al., In: *Handbook of Capillary and Microchip*

Electrophoresis and Associated Microtechniques, Third Edition, James P. Landers (Editor), CRC Press, 2007 (ISBN-10: 0849333296) (Exhibit 8) (underlining added). Similarly, the standard Forensic text by Butler refers to such material as gels: "Prior to injecting each sample, a new gel is 'poured' by filling in the capillary with a fresh aliquot of the polymer solution. The CE can be thought of as a long, skinny gel that is only wide enough for one sample at a time." Forensic DNA Typing Biology, Technology, and Genetics of STR Markers, Second Edition by John Butler, Elsevier, Academic Press, 2005 (p.319) (Exhibit 9) (underlining added).

44. The polyacrylamide gel electrophoresis (or "PAGE") process typically involves the preparation of a polyacrylamide gel between two glass plates, where the gel polymerizes to form a so-called "slab gel." The amplified alleles are then applied to a "well" at the top of the gel, and an electric current is applied to the gel. The amplified alleles will move down the lane below the well, with smaller DNA amplification products (i.e., lower molecular weight products) that contain the amplified STR alleles moving down the gel faster than the larger amplification products (i.e. higher molecular weight products). The various different sizes of the amplification products are separated in this fashion and appear as "bands" on the gel.

45. The alleles from one DNA sample can then be compared to the alleles of a second DNA sample by, for example, running the two samples side-by-side on the gel. One can then determine whether or not the two samples are consistent with coming from the same individual. Additionally a "size marker" or "allelic ladder" is often run concurrently with the sample either mixed with the sample (size marker) or in another lane of the gel

(allelic ladder). By comparing the alleles amplified in the DNA sample to the allelic ladder one can determine precisely which alleles appear in the DNA sample.

46. Like the PAGE technique, separation of the PCR products using capillary gel electrophoresis or CE is based primarily on size. There is nothing in the specifications of the Promega Patents to suggest that the "capillary gel" must be cross-linked. POP-4, which is employed in the examples of the '235 Patent comprises so-called "entangled poly(N,N-dimethylacrylamide)" (or PDMA) which is not cross-linked.

47. The '984 Tautz Patent primarily uses the term "gel" in its unmodified general sense throughout the specification and in the claims. For example Claim 25 is limited only to "a suitable electrophoretic gel," which would be understood by one skilled in the art to include both non-cross-linked (e.g. agarose, entangled PDMA, etc.) and cross-linked gels.

48. The '984 Tautz Patent refers to "direct repeats" and "irregularly direct repeats" (i.e. cryptically simple repeats). A direct repeat is one that is in the same orientation as the index sequence. For example, CAG…..CAG is a direct repeat; CAG…GAC is an inverted repeat. What makes a direct repeat a simple sequence is that it is a tandem repeat. A tandem repeat is a repeat with no intervening nucleotides. For example, CAGCAG is a direct tandem CAG repeat, while CAGTCAG is a non-tandem or irregular direct repeat (i.e. cryptically simple repeat).

49. The underlined portion with arrows underneath in Fig 2 of the Tautz Patent is a simple repeat of 8 base pairs GCTAACTA. There are two tandem copies so it is a simple repeat.

50. For specific CODIS loci examples (Exhibit 10), one can look on the web to determine the repeat structure (see Exhibit 11a through 11n). For example, http://www.cstl.nist.gov/strbase/str_D5S818.htm show the repeat structure for D5S818,

which is a CODIS locus (Exhibit 11d). When one looks at the column listing the "Repeat Structure" one sees that all of the alleles with sequences shown are simple repeats. By contrast, when one looks at http://www.cstl.nist.gov/strbase/str_D21S11.htm, which is D21S11 from CODIS, one finds all of the alleles at this locus are cryptically simple repeats of various types (Exhibit 11m).

51. Below, I briefly review the accused ABI kits and protocols using ABI published materials.

C. ABI/LifeTech Kits and Protocols

ABI/LT Identifiler® Kit

52. The Product Insert for the ABI Identifiler® PCR Amplification Kit (Exhibit 12) lists "PCR Reaction Mix" (which contains the triphosphates in buffer), primer sets, AmpliTaq Gold® DNA Polymerase, and "Control DNA 9947A" among the components of the kit. Clearly these are reagents for performing a PCR amplification reaction. While the control DNA is provided, the test DNA is not in the kit and is in the particular lab where the kit will be used. The primers will anneal to this test DNA as part of the PCR reaction. The kits are indicated as able to "amplify and type" in the context of an ABI PRISM machine. *AmpFlSTR® Identifiler® PCR Amplification Kit, Product P/N 4322288 Insert P/N 4322638 REV G*.

53. The Product Insert for ABI Identifiler® Kit (Exhibit 12) indicates that a certain amount of "input sample DNA" is needed for good results: "The recommended range of input sample DNA is approximately 0.5-1.25 ng. At Applied Biosystems, the kit components have been used successfully to type samples containing less than 0.5 ng of human DNA."

AmpFlSTR® Identifiler® PCR Amplification Kit, Product P/N 4322288 Insert P/N 4322638 REV G [underlining added].

54. The User's Manual for the ABI Identifiler® Kit (Exhibit 13) illustrates the point that samples that possess low amounts of template DNA (i.e. < 0.1ng) are subject to allele drop-out. *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems* [Figure4-12].

55. The User Manual for the ABI Identifiler® Kit (Exhibit 13) indicates the kit permits one to multiplex (i.e. co-amplify) more loci in a single amplification using the "polymerase chain reaction" (PCR): "By adding an additional dye, more loci can be multiplexed in a single PCR amplification as compared to the previous 4-dye system." *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems* pg 1-2 [underlining added].

56. The User Manual for the ABI Identifiler® Kit (Exhibit 13) discusses the degree of amplification of each locus within a "co-amplified" system. *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems* pg 4-34.

57. The User Manual for the ABI Identifiler® Kit (Exhibit 13) makes the distinction between amplifying each locus alone and the situation where the loci are "co-amplified with the *AmpFlSTR* Identifiler kit." *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems* pg 4-36 and pg 4-37.

58. The Product Insert for the Identifier® Kit (Exhibit 12) is identified as providing primers that are covalently labeled: "1 tube containing locus specific 6FAM™, VIC®, NED™, and PET® dye-labeled and unlabeled primers in buffer that amplify the STR loci

CSF1PO, D2S1338, D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D19S433, D21S11, FGA, TH01, TPOX, vWA, and the gender marker, Amelogenin." *AmpFlSTR® Identifiler® PCR Amplification Kit Product P/N 4322288 Insert P/N 4322638 REV G* [underlining added].

59. The User's Manual for the Identifiler® Kit (Exhibit 13) indicates that the dyes are fluorescent labels: "The fluorescent dyes attached to the primers are light-sensitive. Protect the AmpFlSTR Identifiler Primer Set from light when not in use. Amplified DNA, AmpFlSTR® Identifiler™ Allelic Ladder and GeneScan™-500 LIZ™ Size Standard should also be protected from light." *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems* pg 1-7 [underlining added].

60. The User's Manual for the Identifiler® Kit (Exhibit 13) indicates that the kit provides a means to detect separated alleles using fluorescence detection: "The Identifiler kit uses a five-dye fluorescent system for automated DNA fragment analysis." The PCR products are "electrophoretically separated" and "detected" on the ABI PRISM instrument. *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems, pg 1-2 and 3-1. (underlining added).*

61. The Product Insert for the Identifier® Kit (Exhibit 12) is identified as providing an allelic ladder comprising amplified alleles that are covalently labeled: "1 tube of AmpFlSTR® Identifiler® Allelic Ladder containing the following amplified alleles. 6-FAM™ dye (blue): D8S1179 alleles 8-19; D21S11 alleles 24, 24.2, 25-28, 28.2, 29, 29.2, 30, 30.2, 31, 31.2, 32, 32.2, 33, 33.2, 34, 34.2, 35, 35.2, 36-38; D7S820 alleles 6-15; CSF1PO alleles 6-15. VIC® dye (green): D3S1358 alleles 12-19; TH01 alleles 4-9, 9.3, 10, 11,

13.3; D13S317 alleles 8-15; D16S539 alleles 5, 8-15; D2S1338 alleles 15-28. NED™ dye (yellow): D19S433 alleles 9-12, 12.2, 13, 13.2, 14, 14.2, 15, 15.2, 16, 16.2, 17, 17.2; vWA alleles 11-24; TPOX alleles 6-13; D18S51 alleles 7, 9, 10, 10.2, 11-13, 13.2, 14, 14.2, 15-27. PET® dye (red): Amelogenin alleles X and Y; D5S818 alleles 7-16; FGA alleles 17-26, 26.2, 27-30, 30.2, 31.2, 32.2, 33.2, 42.2, 43.2, 44.2, 45.2, 46.2, 47.2, 48.2, 50.2, 51.2." *AmpFlSTR® Identifiler® PCR Amplification Kit Product P/N 4322288 Insert P/N 4322638 REV G* .

62. The User Manual for the ABI Identifiler® Kit (Exhibit 13) indicates the components permit "accurate characterization of the alleles amplified," i.e. permitting one to determine the alleles present: "The AmpFlSTR Identifiler® Allelic Ladder was developed by Applied Biosystems for accurate characterization of the alleles amplified by the AmpFlSTR Identifiler® kit. The AmpFlSTR Identifiler® Allelic Ladder contains the majority of alleles reported for the 15 loci." *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems, pg 3-32* [underlining added].

63. The User Manual for the ABI Identifiler® Kit (Exhibit 13) indicates that the ABI system permits detecting and evaluating amplified alleles: "A ±0.5-bp window allows for the detection and correct assignment of alleles. An allele that sizes only one base pair different from an allele in the allelic ladder will not be incorrectly typed and will be identified as off-ladder." *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems, pg 4-8* [underlining added].

64. The Identifiler® Kit is identified in the User Manual (Exhibit 13) as containing sufficient reagents so as to permit many PCR amplifications: "The AmpFlSTR Identifiler kit

contains sufficient quantities of the following reagents and the appropriate licenses to perform 200 25-µL amplifications …" *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems* pg 1-7 [underlining added].

65. The User's Manual for the Identifiler® Kit (Exhibit 13) indicates that the control DNA can be amplified with the primers to generate "alleles." *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems(Figure3-6).*

66. The User's Manual for the Identifiler® Kit (Exhibit 13) illustrates results obtained when one has a mixture of two samples. Figure 4-16 provides illustrative results for the two samples at different ratios. There is a discussion of using quantitative analysis on these mixtures on page 4-41. Basically, the instrument quantitates the peak heights for each of the amplified alleles, allowing for a comparison. *AmpFlSTR® Identifiler® PCR Amplification Kit User's Manual, Copyright 2006, 2010 Applied Biosystems.*

67. The Product Insert for the Identifiler® Kit (Exhibit 12) identifies a size standard as "Required Materials – Not Included" and describes the size standard as follows:

> GeneScan™-500 LIZ® Size Standard 4322682 2 tubes each containing 200 µL of size standard. Loading buffer is included as a separate tube. GeneScan™-500 LIZ® Size Standard (not GeneScan™-350 ROX™ or GeneScan™-500 ROX™ Size Standards) must be used with the AmpFlSTR® Identifiler® kit.
>
> *AmpFlSTR® Identifiler® PCR Amplification Kit Product P/N 4322288 Insert P/N 4322638 REV G* [underlining added].

ABI/LT Profiler® Kit

68. The Product Insert for the ABI Profiler® PCR Amplification Kit (Exhibit 14) lists "PCR Reaction Mix" (which contains the triphosphates in buffer), primer sets, AmpliTaq Gold® DNA Polymerase, and "Control DNA 9947A" among the components of the kit. A recommended range of "input sample DNA" is set forth. Clearly these are reagents for

performing a PCR amplification reaction. While the control DNA is provided, the test DNA is not in the kit and is in the particular lab where the kit will be used. The primers will anneal to this test DNA as part of the PCR reaction. The kits are indicated as able to "amplify and type" in the context of an ABI PRISM machine. *AmpFlSTR® Profiler® PCR Amplification Kit, Product P/N 403038 Insert P/N 4304212 REV J* .

69. The Product Insert for the ABI Profiler® PCR Amplification Kit (Exhibit 14) indicates that the kit includes dye-labeled primers for nine STR loci (plus a gender marker) in a single tube: "One tube of locus-specific 5-FAM-, JOE-, and NED-labeled and unlabeled primers in buffer to amplify the STR loci D3S1358, vWA, FGA, TH01, TPOX, CSF1PO, D5S818, D13S317, and D7S820, and the gender marker amelogenin. *AmpFlSTR® Profiler® PCR Amplification Kit, Product P/N 403038 Insert P/N 4304212 REV J*.

70. The User's Manual for the ABI Profiler® PCR Amplification Kit (Exhibit 15) indicates that the dyes are fluorescent dyes: "PCR-amplified STR alleles can be detected using various methods, such as fluorescent dye labeling …" *AmpFlSTR® Profiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems, pg 1-1*. (underlining added).

71. The User's Manual for the ABI Profiler® PCR Amplification Kit (Exhibit 15) indicates that the kit employs allelic ladders to type the samples: "The AmpFlSTR Allelic Ladders are used to genotype the analyzed samples. The alleles contained in the allelic ladders and the genotype of the AmpFlSTR Control DNA 9947A are listed in Table 1-3." *AmpFlSTR® Profiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, pg 1-8 [underlining added].

72. The User's Manual for the Profiler® PCR Amplification Kit (Exhibit 15) provides instructions for using the components of the kit to perform a multiplex polymerase chain reaction: "… protocols for PCR amplification of the AmpFlSTR Profiler loci." *AmpFlSTR® Profiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, pg 1-4 [underlining added]

73. The User's Manual for the Profiler® PCR Amplification Kit (Exhibit 15) provides instructions for using the components of the kit to "co-amplify" STR loci: "The AmpFlSTR Profiler PCR Amplification Kit co-amplifies the repeat regions of the following nine short tandem repeat loci …" *AmpFlSTR® Profiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, pg 1-5 [underlining added].

ABI COfiler® Kit

74. The Product Insert for the ABI COfiler® Kit (Exhibit 16) indicates the kit contains "PCR Reaction Mix," dye-labeled primers, DNA polymerase, and "Control DNA 9947A." Clearly these are reagents for performing a PCR amplification reaction. A recommended range of "input sample DNA" is set forth. While the control DNA is provided, the test DNA is not in the kit and is in the particular lab where the kit will be used. The primers will anneal to this test DNA as part of the PCR reaction. The kits are indicated as able to "amplify and type" in the context of an ABI PRISM machine. *AmpFlSTR® COfiler® PCR Amplification Kit, Product P/N 4305246 Insert P/N 4305253 REV K.*

75. The User's Manual for the ABI COfiler® Kit (Exhibit 17) indicates the kit "co-amplifies the repeat regions of the following six tetranucleotide short tandem repeat loci: D3S1358,

D16S539, TH01, TPOX, CSF1PO, and D7S820." *AmpFlSTR® COfiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, pg 1-5.

76. The User's Manual for the ABI COfiler® Kit (Exhibit 17) indicates the kit is to be used "in conjunction with the AmpFlSTR® Profiler Plus™ PCR Amplification Kit to amplify the selected 13 STR loci in two PCR reactions." *AmpFlSTR® COfiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, pg 1-1 (underlining added).

77. The User's Manual for the ABI COfiler® Kit (Exhibit 17) indicates an allelic ladder is provided in the kit and that it "contains the most common alleles for each locus." *AmpFlSTR® COfiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, pg 2-3.

ABI Yfiler® Kit

78. The Product Insert for the ABI Yfiler® Kit (Exhibit 18) lists "PCR Reaction Mix" (with dNTPs in buffer), dye-labeled primer sets, AmpliTaq Gold DNA Polymerase, and "Control DNA 007." Clearly these are reagents for performing a PCR amplification reaction. While the control DNA is provided, the test DNA is not in the kit and is in the particular lab where the kit will be used. The primers will anneal to this test DNA as part of the PCR reaction. The kits are indicated as able to "amplify and type" in the context of an ABI PRISM machine. *AmpFlSTR® Yfiler® PCR Amplification Kit, Product P/N 4359513 Insert P/N 4359563 REV G*.

79. The Product Insert for the Yfiler® PCR Amplification Kit (Exhibit 18) indicates that the kit amplifies 15 STR loci found on the human Y chromosome. *AmpFlSTR® Yfiler® PCR Amplification Kit, Product P/N 4359513 Insert P/N 4359563 REV G*

80. The User's Manual for the Yfiler® PCR Amplification Kit (Exhibit 19) indicates that loci have repeat sequences of 3 to 6 bases that are tandemly repeated. For example, it indicates that the DYS385 14.2 allele contains 14 complete four base pair repeat units and a partial repeat unit of two base pairs. *AmpFlSTR® Yfiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, pg 5-53.

81. The User's Manual for the Yfiler® PCR Amplification Kit (Exhibit 19) indicates the alleles, and these include both simple and cryptically simple DNA sequences. For example, DYS458 contains simple DNA sequence repeats of $[GAAA]_{13}$ to $[GAAA]_{20}$ (http://www.cstl.nist.gov/strbase/str_y458.) *AmpFlSTR® Yfiler® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, p. 6-26.

ABI Profiler Plus®

82. The User's Manual for the ABI Profiler Plus® PCR Amplification Kit (Exhibit 20) indicates the kit "co-amplifies the repeat regions of the following nine short tandem repeat loci: D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, and D7S820" along with a segment of the amelogenin gene. It further indicates that one primer of each locus-specific primer pair is dye labeled so it can be detected on the ABI PRISM instruments." *AmpFlSTR® Profiler Plus® PCR Amplification Kit User's Manual Copyright 2006, 2010 Applied Biosystems*, p. 1-5.

83. Below, I identify the technical elements in the kit claims (section D) and method claims (section E) and find them in the accused products.

D. The Accused Products Have The Technical Elements Specified in the Kit Claims

84. I understand that there is a dispute between the parties concerning whether the claims of the asserted patents, which require the presence of certain identified loci be amplified in

the required multiplex reaction are or are not open-ended, i.e. whether or not primers for additional loci not identified in such claims may also be present in the multiplex reaction. For purposes of this report, I have been asked to assume that such claims are open-ended and that additional loci not identified in such claims may be amplified in the multiplex reaction.

Claim 42 of the '984 Patent

85. I understand that Promega is asserting that a number of claims of the RE37,984 Patent are infringed by Life Tech/ABI when certain products are sold (outside the licensed fields). Claim 42 is a kit claim which specifies five (5) elements:

    a) a vessel comprising a mixture of primers,

    b) a vessel containing a polymerase,

    c) a vessel containing triphosphates,

    d) a vessel containing a buffer and

    e) a vessel containing control template DNA comprising i) simple or cryptically simple repeats, the repeat motif of 3 to 10 nucleotides in length and ii) flanking sequences for annealing at least one pair of primers.

All of the accused products provide these reagents. As noted above (paragraph 52), the Identifiler® Kit lists "PCR Reaction Mix" (which contains the triphosphates in buffer), along with a) primer sets to amplify STR loci, b) AmpliTaq Gold® DNA Polymerase, and e) control DNA. As noted above, the COfiler® Kit (see paragraph 74) and Yfiler® Kit (paragraph 75) contain these components. The Profiler® Kit also contains these reagents (paragraph 68). To the extent the triphosphates and buffer in these kits are not in separate

vessels, there is no significant technical difference, since they will all eventually be mixed together in the reaction.

86. Part e) of Claim 42 of the '984 Patent indicates that the template DNA in the kit must be such that repeats of 3 to 10 nucleotides in length can be amplified with the primers in the kit (although no specific loci are mentioned in Claim 42). As noted above, the accused ABI/LT kits contain control DNA template which the primers can amplify. More specifically, as noted above (paragraph 65), the User's Manual for the Identifiler® Kit (Exhibit 13) indicates that the control DNA can be amplified with the primers to generate "alleles."

87. Part e) of Claim 42 specifies repeats and repeat "motifs" (a term I explained above, at paragraph 31). All of the accused products amplify a locus which has either simple or cryptically simple sequence repeats. For example, the COfiler® Kit includes the TPOX locus among the loci amplified. The TPOX locus has many alleles which are simple $(AATG)_n$ repeats. In addition, the Identifiler® Kit and the Profiler Plus® Kit include the D21S11 locus among the loci amplified (as noted previously at paragraph 50, all of the alleles at this locus are cryptically simple repeats of various types). The Identifier® Kit, the Profiler® Kit, and the Profiler Plus® Kit include the D5S818 locus among the loci amplified (as noted previously at paragraph 50, all of the alleles with sequences shown are simple repeats). The alleles amplified by the Yfiler® PCR Amplification Kit have repeat sequences of 3 to 6 bases that are tandemly repeated; the alleles include both simple and cryptically simple DNA sequences (see paragraphs 77-79, above). Therefore, I conclude that the accused products provide the technical elements set forth in Claim 42 of the '984 Patent.

Claim 5 of the '771 Patent

88. I understand that the only asserted Claim of U.S. Patent No. 7,008,771 is Claim 5 and that Promega asserts this claim is directly infringed by the Life Tech/ABI Identifiler® product (when sold outside the licensed fields). Claim 5 is a kit claim which recites in part: "A kit for simultaneously analyzing a set of loci of genomic DNA, comprising oligonucleotide primers for co-amplifying a set of loci of the Genomic DNA to be analyzed, wherein the primers are in one or more containers, wherein the primers are designed to co-amplify a set of loci from one or more DNA samples, comprising short tandem repeat loci . . . [list of 13 particular loci] and a locus selected from the group consisting of G475 . . .and Amelogenin." (Claim 5, underlining added).

89. I have looked at the technical elements specified in Claim 5. Claim 5 specifies 13 particular loci (along with an additional locus which can be Amelogenin) to be co-amplified. The Life Tech/ABI Identifiler® product is indicated to be a "Fluorescent STR kit" that includes, among other things, primers for co-amplifying "15 STR loci" which include the 13 recited STR loci in Claim 5 and the Amelogenin locus (see paragraphs 58-59, above). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 5 of the '771 Patent. (see Chart 1, attached hereto).

90. So that there is no confusion, I note that, while Claim 5 specifies "HUMCSF1PO," HUMTH01," and "HUMTPOX," these loci are also known simply as CSF1PO, TH01 and TPOX. While Claim 5 specifies "HUMFIBRA," this locus is also known simply as FGA. While Claim 5 specifies HUMvWFA31," this locus is also known simply as vWA. The ABI kits use the shorter name for these loci.

Claims 18-19 and 21-23 of the '235 Patent

91. I understand that Promega asserts that Claims 1, 4, 6-13, 15-19, and 21-23 of U.S. Patent No. 6,479,235 are directly infringed by the Life Tech/ABI Identifiler® product (when sold outside the licensed fields). I have looked at the technical elements specified in these claims. Claim 18 is a kit claim which recites in part: "A kit for simultaneously analyzing a set of loci of genomic DNA comprising oligonucleotide primers for co-amplifying a set of loci of the genomic DNA to be analyzed, wherein the set of loci comprises short tandem repeat loci which can be co-amplified, the primers are in one or more containers, the genomic DNA is human genomic DNA, and the loci comprise . . . . [list of 13 particular loci]. (Claim 18, underlining added). Claim 18 specifies 13 particular loci to be co-amplified. The Life Tech/ABI Identifiler® product is indicated to be a "Fluorescent STR kit" that includes, among other things, primers for co-amplifying "15 STR loci" which include the 13 required STR loci in Claim 18. (see Chart 2, attached hereto). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 18 of the '235 Patent.

92. So that there is no confusion, I again note that, while Claim 18 specifies "HUMCSF1PO," HUMTH01," and "HUMTPOX," these loci are also known simply as CSF1PO, TH01 and TPOX. While Claim 18 specifies "HUMFIBRA," this locus is also known simply as FGA. While Claim 18 specifies HUMvWFA31," this locus is also known simply as vWA. The ABI kit refers to the short name for these loci.

93. Claim 19 of the '235 Patent depends on Claim 18 and adds the feature that all of the primers are in one container. As noted previously, the primers in the Identifiler® product

kit are in "one tube" (paragraph 58, above). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 19 of the '235 Patent.

94. Claim 21 of the '235 Patent depends on Claim 18 and adds the feature of "reagents for at least one multiplex amplification reaction." Such reagents would include a polymerase and triphosphates. As noted above (paragraph 52), the Identifiler® Kit contains such reagents. Therefore, I conclude that the accused product provides the technical elements set forth in Claim 21 of the '235 Patent.

95. Claim 22 of the '235 Patent depends on Claim 18 and adds the feature of an "allelic ladder." The Identifiler® Kit also specifies an "Allelic Ladder" (see paragraph 61, above). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 22 of the '235 Patent.

96. Claim 23 of the '235 Patent depends on Claim 22 and adds the feature that the rungs of the allelic ladder and at least one primer have a fluorescent label covalently attached, and at least two primers have different labels. The Identifier® Kit provides allelic ladder rungs and primers that are covalently labeled with fluorescent dyes, including primers with different labels (see paragraphs 58-61, above). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 23 of the '235 Patent.

Claim 25 and 27-31 of the '660 Patent

97. I understand that Promega asserts that Claims 2-5, 9, 16-17, 19-21, 23-25, and 27-31 of U.S. Patent No. 5,843,660 are directly infringed by the Life Tech/ABI Identifiler® product (when sold outside the licensed fields). I have looked at the technical elements specified in these claims. Claim 25 is a kit claim which recites in part: "A kit for simultaneously analyzing short tandem repeat sequences in at least three loci, comprising

a container which has oligonucleotide primers for co-amplifying a set of at least three short tandem repeat loci, wherein the set of loci are selected from the sets of loci consisting of: [list of 29 sets of loci]. (Claim 25, underlining added). While 29 sets of loci are set forth in Claim 25, one of the 29 sets specifies that the three loci are D16S539, D7S820, and D13S317. As noted above, the Identifiler® Kit primers in a single tube (paragraph 58) to co-amplify loci combinations including D7S820, D13S317, and D16S539. (see Chart 3). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 25 of the '660 Patent.

98. Claim 27 depends on Claim 25 and further specifies "a container having reagents for at least one multiplex amplification reaction." As noted above, the Identifiler® Kit provides multiplex amplification reaction reagents (paragraph 52). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 27 of the '660 Patent.

99. Claim 28 depends on Claim 25 and further specifies "a container having an allelic ladder." As noted previously, the Identifiler® Kit provides a container having an allelic ladder (paragraph 61). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 28 of the '660 Patent.

100. Claim 29 depends on Claim 28 and further specifies "each rung of the allelic ladder and at least one primer … have a label covalently attached." As noted previously, the Identifiler® Kit provides allelic ladder rungs and primers that are covalently labeled (see paragraphs 58-61, above). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 29 of the '660 Patent.

101. Claim 30 depends on Claim 29 and further specifies "the label is a fluorescent label." As noted previously, the Identifiler® Kit provides reagents with fluorescent labels (see

paragraphs 58-61). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 30 of the '660 Patent.

102. Claim 31 depends on Claim 30 and further specifies "at least one of the … primers … has a different fluorescent label …". As noted previously, the Identifier® Kit provides at least one primer fluorescent label that is different from another primer fluorescent label (see paragraphs 58-61). Therefore, I conclude that the accused product provides the technical elements set forth in Claim 31 of the '660 Patent.

Claims 10, 23-24, 27 and 33 of the '598 Patent

103. I understand that Promega asserts that Claims 1-2, 4-10, 12, 15, 19, 21-24, 27-28, and 31-33 of U.S. Patent No. 6,221,598 are directly infringed by some ABI products, including the Life Tech/ABI Identifiler® product and Profiler® Kit (when sold outside the licensed fields). I have looked at the technical elements specified in these claims. Claim 10 is a kit claim which recites in part: "A kit for simultaneously analyzing short tandem repeat sequences in at least three loci, comprising: a single container containing oligonucleotide primers for each locus in a set of at least three short tandem repeat loci, wherein the at least three short tandem repeat loci in the set comprises at least three loci selected from the group consisting of: [list of 20 sets of loci]. (Claim 10, underlining added). While 20 different sets of loci are listed in Claim 10, one set specifies that the loci include at least HUMTPOX, HUMVWFA31 and HUMCSF1PO (in a first case), and (in another case) HUMCSF1PO, HUMTH01 and HUMVWFA31 (among a number of possible sets). As noted previously, simpler names for these loci are TPOX, vWA and CSF1PO (in the one case) and CSF1PO, TH01 and vWA (in the other). The Identifiler® Kit and the Profiler® Kit provide a single container with primers for these three loci (as well as additional loci)

(see Charts 4a and 4b). Therefore, I conclude that the Identifiler® Kit and the Profiler® Kit provide the technical elements set forth in Claim 10 of the '598 Patent.

104. Claim 23 of the '598 Patent is also a kit claim which specifies in part: "A kit for simultaneously analyzing short tandem repeat sequences in a set of short tandem repeat loci from one or more DNA samples, comprising: a single container containing oligonucleotide primers for each locus in a set of short tandem repeat loci which can be co-amplified, comprising, HUMCSF1PO, HUMTPOX and HUMTH01." (Claim 23, underlining added). Claim 23 indicates the loci include HUMCSF1PO, HUMTPOX, and HUMTH01 (or more simply, CSF1PO, TPOX and TH01). The COfiler® Kit co-amplifies TPOX, TH01 and CSF1PO (along with other loci) which are the loci specified in Claim 23 (see Chart 5). The Identifiler® Kit and the Profiler® Kit provide a single container with primers for these three loci (as well as additional loci) (see Chart 5). Therefore, I conclude that the Identifiler® Kit, COfiler® Kit and the Profiler® Kit provide the technical elements set forth in Claim 23 of the '598 Patent.

105. Claim 24 depends on Claim 23 and further specifies that the kit contains primers designed to co-amplify the HUMVWFA31 (or more simply vWA) locus. The Identifiler® Kit (see paragraph 58) and the Profiler® Kit (see paragraph 69) are identified as providing a single container with primers for this locus as well. Therefore, I conclude that the Identifiler® Kit and the Profiler® Kit provide the technical elements set forth in Claim 24 of the '598 Patent.

106. Claims 27 depends on Claim 23 and specifies "at least one of each of the pair of oligonucleotide primers in the kit is fluorescently-labeled." As noted previously, the Identifiler® Kit (see paragraphs 58-59), the COfiler® Kit (see paragraph 74) and the

Profiler® Kit (see paragraphs 69-70) are identified as providing fluorescently labeled primers. Therefore, I conclude that the Identifiler® Kit and the Profiler® Kit provide the technical elements set forth in Claim 27 of the '598 Patent.

107. Claim 33 is another independent kit claim of the '598 Patent and it recites in part: "A kit for simultaneously analyzing short tandem repeat sequences in a set of short tandem repeat loci from one or more DNA samples, comprising: a single container containing oligonucleotide primers for each locus in a set of short tandem repeat loci which can be co-amplified, comprising, HUMTPOX, HUMVWFA31, and HUMCSF1PO." (Claim 33, underlining added). Claim 33 indicates that the loci include HUMCSF1PO, HUMTPOX and HUMVWFA31 (or more simply, CSF1PO, TPOX and vWA). The Identifiler® Kit (see paragraph 58) and the Profiler® Kit (see paragraph 69) are identified as providing a single primer container for these loci (see Chart 6). Therefore, I conclude that the Identifiler® Kit and the Profiler® Kit provide the technical elements set forth in Claim 33 of the '598 Patent.

E. The Accused Products Have The Technical Elements Specified in the Method Claims

Claims 15-16, 18, 23, 25, 27-28 and 41 of the '984 Patent

108. I understand that Promega is asserting that a number of method claims of the RE37,984 Patent are infringed by Life Tech/ABI when certain products are sold (outside the licensed fields). Claim 15 is a method claim which recites in part: "A method for analyzing length polymorphisms in at least one locus in an DNA sample . . . wherein said

DNA sample comprises a DNA template having at least one locus comprising a simple or cryptically simple DNA sequence, said method comprising:

a) annealing said DNA template with at least one pair of primers, wherein said primer pair is composed of a first primer complementary to a nucleotide sequence flanking said simple or cryptically simple DNA sequence on the 5' side of said simple or cryptically simple DNA sequence and a second primer complementary to a nucleotide sequence flanking the simple or cryptically simple DNA sequence on the 3' side of said simple or cryptically simple DNA sequence; wherein said first and second primers each anneal to a single site in said DNA template and wherein the annealing sites are separated by 50 to 500 nucleotides of template DNA;

b) performing at least one primer-directed polymerase chain reaction upon said template DNA having said primers annealed thereto, so as to form at least one polymerase chain reaction product;

c) separating the products of each polymerase chain reaction according to their lengths; and

d) analyzing the lengths of the separated products to determine the length polymorphisms of said simple or cryptically simple sequences; wherein said simple or cryptically simple sequence has a repeat length of 3 to 10 nucleotides.

I have discussed the meaning of "simple" and "cryptically simple sequences" shown underlined above (see paragraphs 48-50). As noted above in the context of Claim 42 of

the '984 Patent, all of the accused products amplify a locus which has either simple or cryptically simple sequence repeats. For example, the COfiler® Kit includes the TPOX locus among the loci amplified. The TPOX locus has many alleles which are simple $(AATG)_n$ repeats. In addition, the Identifiler® Kit and the Profiler Plus® Kit (see paragraph 82) include the D21S11 locus among the loci amplified (as noted previously at paragraph 50, all of the alleles at this locus are cryptically simple repeats of various types). The Identifier® Kit, the Profiler® Kit, and the Profiler Plus® Kit include the D5S818 locus among the loci amplified (as noted previously at paragraph 50, all of the alleles with sequences shown are simple repeats). The alleles amplified by the Yfiler® PCR Amplification Kit have repeat sequences of 3 to 6 bases that are tandemly repeated; the alleles include both simple and cryptically simple DNA sequences (see paragraphs 77-79, above).

109. I have also discussed the steps of a) annealing and b) performing a PCR reaction, (see underlining in Claim 15 above) in general terms previously (see paragraphs 30-33, 35-37). These steps are specified for users of the accused kits. For example, the COfiler® Kit is a PCR amplification kit with primers for annealing, as part of the PCR reaction (see paragraph 74). Similarly, the Identifiler® Kit (paragraph 52) and the Profiler® Kit (paragraph 68) provide reagents for PCR, including primers for annealing to template as part of the PCR reaction. Finally, the Yfiler® Kit is a PCR amplification kit with primers for annealing, as part of the PCR reaction (see paragraph 76).

110. I have also discussed the steps of c) separating the PCR products, and d) analyzing the separated products to determine length polymorphisms which are underlined above in Claim 15 (see paragraphs 41, and 45-46). These steps are specified for users of the

accused kits. For example, the COfiler® Kit is a PCR amplification kit which is indicated as able to "amplify and type" in the context of an ABI PRISM machine (see paragraph 74). The Yfiler® Kit is a PCR amplification kit which is indicated as able to "amplify and type" in the context of an ABI PRISM machine (see paragraph 74). Similarly, the Identifiler® Kit (paragraphs 52) and the Profiler® Kit (paragraph 68) are indicated as able to "amplify and type" in the context of an ABI PRISM machine. The User Guide for the Identifiler® Kit indicates that the PCR products are "electrophoretically separated" and "detected" on the ABI PRISM instrument. Therefore, I conclude that the Identifiler® Kit, the Profiler® Kit, the Profiler Plus® Kit, the Yfiler® Kit, and the COfiler® Kit all provide the technical elements set forth in Claim 15 of the '984 Patent.

111. Claim 16 of the '984 Patent depends on Claim 15 and further specifies that the repeat length is between 3 and 6 nucleotides. I discussed repeat lengths of the loci amplified by the kits in the context of the length range of 3 to 10 nucleotides for Claim 15 (see paragraph 104). Claim 16 simply is a narrower range. Nonetheless, the kits amplify loci with repeat lengths in this range. For example, as noted previously, the alleles amplified by the Yfiler® PCR Amplification Kit have repeat sequences of 3 to 6 bases that are tandemly repeated; the alleles include both simple and cryptically simple DNA sequences (see paragraphs 77-79, above). Therefore, I conclude that the Identifiler® Kit, the Profiler® Kit, the Profiler Plus® Kit, the Yfiler® Kit, and the COfiler® Kit all provide the technical elements set forth in Claim 15 of the '984 Patent.

112. Claim 18 of the '984 Patent depends on Claim 15 and further specifies that "at least two primer pairs are used." As noted previously, the accused kits have many primer pairs for amplification of many loci (see paragraphs 58, 69, 75, 77, and 82 above). Therefore, I

conclude that the Identifiler® Kit, the Profiler® Kit, the Profiler Plus® Kit, the Yfiler® Kit, and the COfiler® Kit all provide the technical elements set forth in Claim 18 of the '984 Patent.

113. Claim 23 of the '984 Patent depends on Claim 15 and further specifies that "2 to 50 primer pairs are used." As noted previously, the accused kits have primer pairs for amplification of loci, the number of which falls within this range (see paragraphs 58, 69, 75, 77, and 82 above). Therefore, I conclude that the Identifiler® Kit, the Profiler® Kit, the Yfiler® Kit, the Profiler Plus® Kit, and the COfiler® Kit all provide the technical elements set forth in Claim 23 of the '984 Patent.

114. Claim 25 depends on Claim 15 and further specifies that "each of the products of the primer-directed polymerase chain reaction is separable one from the other as individual bands on a suitable electrophoretic gel." As noted above, each of the accused products is able to amplify and type in the context of an ABI PRISM instrument (see paragraphs 52, 68, 74, 76 and 82) and this instrument is used to "electrophoretically separate" and "detect" the amplified products using a "five-dye fluorescent system" (see paragraph 60). Thus, size and color signal are used together to separate "one from the other."

115. Claim 27 depends on Claim 15 and specifies that the PCR product "is labeled by a non-radioactive label." As noted above, each of the accused products utilizes dye-labeled primers (see paragraphs 58, 69, 74, 76 and 82), which will generate a PCR product labeled with a non-radioactive label. Therefore, I conclude that the Identifiler® Kit, the Profiler® Kit, the Yfiler® Kit, the Profiler Plus® Kit, and the COfiler® Kit all provide the technical elements set forth in Claim 27 of the '984 Patent.

116. Claim 28 depends on Claim 27 and specifies that the "non-radioactive label is a fluorescent label." As noted above, each of the accused products utilizes dye-labeled primers (see paragraphs 58, 69, 74, 76, and 82). Moreover, these dyes are fluorescent (see paragraphs 59 and 70). Therefore, I conclude that the Identifiler® Kit, the Profiler® Kit, the Yfiler® Kit, the Profiler Plus® Kit, and the COfiler® Kit all provide the technical elements set forth in Claim 28 of the '984 Patent.

117. Claim 41 of the '984 Patent is a method claim which recites in part: "A method for analyzing polymorphism in at least one locus in an DNA sample comprising a DNA template, said method comprising:

a) annealing said DNA template with at least one pair of primers, . . .

b) performing at least one primer-directed polymerase chain reaction upon said template DNA having said primers annealed thereto, so as to form at least one polymerase chain reaction product;

c) separating the products of each polymerase chain reaction product according to their lengths; and

d) analyzing the lengths of the separated products to determine the length polymorphisms of said simple or cryptically simple sequences, wherein said DNA template includes at least one sequence consisting essentially of a simple or cryptically simple DNA sequence having a repeat motif length of 3 to 10 nucleotides and nucleotide sequences flanking said simple or cryptically simple DNA sequence effective for annealing said at least one pair of primers."

I have discussed the meaning of "simple" and "cryptically simple sequences" shown underlined above (see paragraphs 48-50). As noted above in the context of Claim 42 of the '984 Patent, all of the accused products amplify a locus which has either simple or cryptically simple sequence repeats. For example, the COfiler® Kit includes the TPOX locus among the loci amplified. The TPOX locus has many alleles which are simple $(AATG)_n$ repeats. In addition, the Identifiler® Kit and the Profiler Plus® Kit include the D21S11 locus among the loci amplified (as noted previously at paragraph 50, all of the alleles at this locus are cryptically simple repeats of various types). The Identifier® Kit, the Profiler® Kit, and the Profiler Plus® Kit include the D5S818 locus among the loci amplified (as noted previously at paragraph 50, all of the alleles with sequences shown are simple repeats). The alleles amplified by the Yfiler® PCR Amplification Kit have repeat sequences of 3 to 6 bases that are tandemly repeated; the alleles include both simple and cryptically simple DNA sequences (see paragraphs 77-79, above).

118. I have also discussed the steps of a) annealing and b) performing a PCR reaction, (see underlining in Claim 41 above) in general terms previously (see paragraphs 30-33, 35-37). These steps are specified for users of the accused kits. For example, the COfiler® Kit is a PCR amplification kit with primers for annealing, as part of the PCR reaction (see paragraph 74). Similarly, the Identifiler® Kit (paragraph 52) and the Profiler® Kit (paragraph 68) provide reagents for PCR, including primers for annealing to template as part of the PCR reaction. Finally, the Yfiler® Kit is a PCR amplification kit with primers for annealing, as part of the PCR reaction (see paragraph 76).

119. I have also discussed the steps of c) separating the PCR products, and d) analyzing the separated products to determine length polymorphisms which are underlined above in

Claim 41 (see paragraphs 41, and 45-46). These steps are specified for users of the accused kits. For example, the COfiler® Kit is a PCR amplification kit which is indicated as able to "amplify and type" in the context of an ABI PRISM machine (see paragraph 74). The Yfiler® Kit is a PCR amplification kit which is indicated as able to "amplify and type" in the context of an ABI PRISM machine (see paragraph 74). Similarly, the Identifiler® Kit (paragraphs 52) and the Profiler® Kit (paragraph 68) are indicated as able to "amplify and type" in the context of an ABI PRISM machine. The User Guide for the Identifiler® Kit indicates that the PCR products are "electrophoretically separated" and "detected" on the ABI PRISM instrument. Therefore, I conclude that the Identifiler® Kit, the Profiler® Kit, the Profiler Plus® Kit, the Yfiler® Kit, and the COfiler® Kit all provide the technical elements set forth in Claim 41 of the '984 Patent.

Claims 1, 12 and 28 of the '598 Patent (and dependent claims)

120. Claims 1, 12, and 28 are independent method claims of the '598 Patent. Claim 1 recites in part a method having the following steps:

a) obtaining at least one DNA sample to be analyzed;

b) selecting a set of at least three short tandem repeat loci of the DNA sample to be analyzed which can be co-amplified, wherein the at least three short tandem repeat loci in the set comprises at least three loci selected from the group consisting of: [list of 18 sets of loci];

c) co-amplifying . . . thereby producing a mixture of amplified alleles . . .; and

d) evaluating the amplified alleles . . . to determine the alleles present at each of the co-amplified loci in the set.

Claim 12 is similar to Claim 1, but differs in that it only sets forth a single set of loci. Claim 12 recites in part:

a) obtaining at least one DNA sample to be analyzed;

b) selecting a set of short tandem repeat loci of the DNA sample to be analyzed which can be co-amplified, comprising HUMCSF1PO, HUMTPOX, and HUMTH01;

c) co-amplifying the set of short tandem repeat loci in a multiplex amplification reaction, thereby producing a mixture of amplified alleles from each of the co-amplified loci in the set; and

d) evaluating the amplified alleles in the mixture to determine the alleles present at each of the co-amplified loci in the set.

Claim 28 is similar to Claim 12 in that it also sets forth only a single set of loci. Claim 28 recites in part:

a) obtaining at least one DNA sample to be analyzed;

b) selecting a set of short tandem repeat loci of the DNA sample to be analyzed which can be co-amplified, comprising HUMTPOX, HUMVWFA31, and HUMCSF1PO;

c) co-amplifying the set of short tandem repeat loci in a multiplex amplification reaction, thereby producing a mixture of amplified alleles from each of the co-amplified loci in the set; and

d) evaluating the amplified alleles in the mixture to determine the alleles present at each of the co-amplified loci in the set.

121. From the above, it is clear that Claims 1, 12 and 28 have some common steps with some language in common (which is underlined above):

Step a)

Claims 1, 12, 28 at step a) specify "obtaining at least one DNA sample." All products accused of infringing the '598 Patent utilize at least one DNA sample in their protocols. Indeed, the Identifiler® Kit, the Profiler® Kit, and the COfiler® Kit all provide a recommended range of "input sample DNA." (paragraphs 53, 68 and 74, above). Therefore, I conclude that the technical elements for step a) of these claims are found in the accused kits.

Step b)

Claims 1, 12 and 28 specify at step b) "selecting a set of . . . short tandem repeat loci … which can be co-amplified." Specifically, claim 1 specifies in step b) that the "at least three loci selected" are from a group which includes in one case HUMTPOX, HUMTH01, and HUMVWFA31, and in another case HUMCSF1PO, HUMTH01, and HUMVWFA31 (among a number of possible sets of loci listed). Claim 12 specifies in step b) that the set of loci selected comprises HUMCSF1PO, HUMTPOX, and HUMTH01. Claim 28 specifies in step b) that the set of loci selected comprises HUMTPOX, HUMVWFA31, and HUMCSF1PO. All products accused of infringing the '598 Patent utilize at least three short tandem repeat loci which can be co-amplified in their protocols. The COfiler® Kit co-amplifies TPOX, TH01 and CSF1PO (along with other loci) (see Chart 7), which is the precise combination specified in Claim 12. The Identifiler® Kit (paragraph 58) and the Profiler® Kit (paragraph 69) are identified as co-

amplifying short tandem repeat loci which include these loci (see Chart 8a and 8b) (see Chart 9). Therefore, I conclude that the technical elements for step b) of these claims are found in the accused kits.

Step c)

Claims 1, 12 and 28 further specify at step c) "co-amplifying . . . , thereby producing a mixture of amplified alleles . . ." I have discussed the meaning of amplifying and "co-amplifying" (see paragraphs 32-33, above). I have also noted that the Identifiler® Kit (see paragraphs 55-57), the COfiler® Kit (paragraph 75), and the Profiler® Kit (paragraph 73) all "co-amplify" to produce a mixture of alleles. Therefore, I conclude that the technical elements for step c) of these claims are found in the accused kits.

Step d)

Claims 1, 12 and 28 further specify at step d) evaluating the amplified alleles . . . to determine the alleles present . . ." I have previously indicated that the Identifiler® Kit (see paragraph 52), the COfiler® Kit (paragraph 74), and the Profiler® Kit (paragraph 68) are able to "amplify and type" in the context of an ABI PRISM machine and thereby accurately characterize the alleles present (paragraph 62). Therefore, I conclude that the technical elements for step d) of these claims are found in the accused kits.

122. Claim 2 of the '598 depends on Claim 1 and specifies that the loci "are co-amplified by multiplex polymerase chain reaction." I have discussed the difference between a "monoplex" (paragraph 39) and a multiplex (paragraph 40). The User Manual for the ABI Identifiler® Kit (Exhibit 13) makes this distinction (paragraph 57). I have previously

indicated that the Identifiler® Kit (see paragraph 52), the COfiler® Kit (paragraph 74), and the Profiler® Kit (paragraph 68) provide reagents for performing a PCR amplification reaction. Therefore, I conclude that the technical elements for Claim 2 of the '598 are found in the accused kits.

123. Claim 4 of the '598 depends on Claim 1 and specifies that the alleles are evaluated by comparing the alleles to a size standard or a locus-specific allelic ladder. I have previously indicated that the Identifiler® Kit (see paragraph 61-62), the COfiler® Kit (paragraph 77), and the Profiler® Kit (paragraph 71) each provide an allelic ladder the most common alleles for each locus (i.e. it is locus specific). The kits also list a size standard as "required materials" (see e.g. paragraph 67). Therefore, I conclude that the technical elements for Claim 4 of the '598 are found in the accused kits.

124. Claims 15 and 21 of the '598 specify that the set of loci co-amplified further comprises HUMVWFA31. I have noted previously (paragraph 89) that this locus is also known simply as vWA. The ABI kit refers to the short name for this locus. The Identifiler® Kit (paragraph 58) and the Profiler® Kit (paragraph 69) also co-amplify this locus. Therefore, I conclude that the technical elements for Claim 15 of the '598 are found in the accused kits.

125. Claim 19 depends on Claim 12 and specifies "oligonucleotide primers for each locus in the set of loci selected in step (b), wherein at least one of the oligonucleotide primers for each locus is fluorescently labeled." The Identifiler® Kit (paragraph 52), the COfiler® Kit (paragraph 74) and the Profiler® Kit (paragraph 68) provide oligonucleotide primers for each locus. The Identifiler® Kit (paragraph 58-59), COfiler® Kit (paragraph 74) and the Profiler® Kit (paragraph 69-70) indicate the primers are fluorescently labeled. Therefore,

I conclude that the technical elements for Claim 19 of the '598 are found in the accused kits.

Claims of the 660 Patent

126. Claim 16 of the '660 is a method claim which reads in part: "comprising:

(a) obtaining at least one DNA sample to be analyzed,

(b) selecting a set of three short tandem repeat loci of the DNA sample to be analyzed which can be amplified together, wherein the set of three loci is selected from the group of sets of loci consisting of [six sets of loci];

(c) co-amplifying the three loci in the set in a multiplex amplification reaction, wherein the product of the reaction is a mixture of amplified alleles from each of the co-amplified loci in the set; and

(d) evaluating the amplified alleles in the mixture to determine the alleles present at each of the loci analyzed in the set within the DNA sample. Claim 1 (not asserted) of the '660 is similar except for the fact that it specifies "a set of at least four short tandem repeat loci."

127. Claims 2, 3, 4 and 5, each of which depends on Claim 1 (not asserted), and claim 16 each specify at step (a) "obtaining at least one DNA sample . . .". I have previously noted that the kits utilize at least one DNA sample in their protocols. Indeed, the Identifiler® Kit provides a recommended range of "input sample DNA." (see paragraphs 53, above). Therefore, I conclude that the technical elements for step a) of these claims are found in the accused kit.

128. Claims 2, 3, 4 and 5 and 16 specify the following at step b):

Claim 2: selecting "a set of at least four loci" from a "group of sets of loci" that include in one case "D7S820, D13S317, D16S539, HUMvWFA31."
Claim 3: selecting "a set of at least six loci" from a "group of sets of loci" that include in, one case, "D16S539, D7S820, D13S317, D5S818, HUMCSF1PO, and HUMTPOX."
Claim 4: selecting "a set of at least seven loci" from a "group of sets of loci" that include in, one case, "D16S539, D7S820, D13S317, D5S818, HUMCSF1PO, HUMTPOX, and HUMTH01."
Claim 5: selecting "a set of at least eight loci" from a "group of sets of loci" that include in, one case, "D16S539, D7S820, D13S317, D5S818, HUMCSF1PO, HUMTPOX, HUMTH01 and HUMvWFA31."
Claim 16: selecting "a set of at least three loci" from a "group of sets of loci" that include in, one case, "D16S539, D7S820, D13S317."

The Identifiler® Kit co-amplifies loci that include each of the above identified sets of loci regarding claims 2-5 and 16 (see paragraph 58, above) (see Charts 10 through 14). Therefore, I conclude that the technical elements for step b) of these claims are found in the accused kit.

129. Claims 2-5 and 16 further specify at step c) "co-amplifying . . ." I have discussed the meaning of amplifying and "co-amplifying" (see paragraphs 32-33, above). I have also noted that the Identifiler® Kit (see paragraphs 55-57) "co-amplifies" to produce a mixture of alleles. Therefore, I conclude that the technical elements for step c) of these claims are found in the accused kit.

130. Claims 2-5 and 16 further specify at step d) evaluating the amplified alleles . . . to determine the alleles present . . ." I have previously indicated that the Identifiler® Kit (see paragraph 52) is able to "amplify and type" in the context of an ABI PRISM machine and thereby accurately characterize the alleles present (paragraph 62). Therefore, I conclude that the technical elements for step d) of these claims are found in the accused kit.

131. Claim 17, which depends on claim 16, specifies that "the amplification is done using three pair of primers, wherein each pair of primers flanks one of the three short tandem repeat loci." I have previously discussed the meaning of flanking regions (see paragraph 3 above). The Identifiler® Kit uses primers which flank the repeating sequence. Otherwise they could not amplify the STR loci they claim as referenced above.

132. Claim 19 depends on Claim 16 and specifies that "the multiplex reaction is a polymerase chain reaction". I have discussed the difference between a "monoplex" (paragraph 39) and a multiplex (paragraph 40). The User Manual for the ABI Identifiler® Kit (Exhibit 13) makes this distinction (paragraph 57). I have previously indicated that the Identifiler® Kit (see paragraph 52) provide reagents for performing a PCR amplification reaction. Therefore, I conclude that the technical elements for Claim 19 of the '660 are found in the accused kit.

133. Claim 20 is dependent from Claim 16 and specifies "comparing separated alleles to a size standard, wherein the size standard is selected from a group of size standards consisting of a DNA marker and a locus-specific allelic ladder. " I have previously indicated that the Identifiler® Kit (see paragraph 61-62) provides an allelic ladder comprising the most common alleles for each locus (i.e. it is locus specific). The kits also list a size standard as "required materials" (see e.g. paragraph 67). Therefore, I conclude that the technical elements for Claim 20 of the '660 are found in the accused kit.

Claims of the '235 Patent

134. Claims 1 and 13 of the '235 Patent are methods claims. Claim 1 of the '235 patent reads in part:

(a) obtaining at least one DNA sample to be analyzed,

(b) selecting a set of loci of the DNA sample, comprising D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, HUMCSF1PO, HUMFIBRA, HUMTH01, HUMTPOX, and HUMvWFA31,

(c) co-amplifying the loci in the set in a multiplex amplification reaction, wherein the product of the reaction is a mixture of amplified alleles from each of the co-amplified loci in the set; and

(d) evaluating the amplified alleles in the mixture to determine the alleles present at each of the loci analyzed in the set within the DNA sample.

135. Claim 13 of the '235 Patent reads in part:

a) obtaining at least one DNA sample to be analyzed;

b) selecting a set of loci of the DNA sample, comprising short tandem repeat loci D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, HUMCSF1PO, HUMFIBRA, HUMTH01, HUMTPOX, and HUMvWFA31;

c) co-amplifying the loci in the set in a multiplex amplification reaction, wherein the product of the reaction is a mixture of amplified alleles from each of the co-amplified loci in the set; and

d) evaluating the amplified alleles in the mixture to determine the alleles present at each of the loci analyzed in the set within the DNA sample.

136. With regard to step a) of Claim 1 and 13 of the '235 Patent, I have previously indicated that the Identifiler® Kit provides a recommended range of "input sample DNA." (see paragraphs 53, above). With regard to step b) of Claim 1 and 13 of the '235 Patent, I

have previously indicated the Identifiler® Kit (paragraph 58) provides primers to amplify the loci of step b) (see Charts 15 and 16). With regard to step c) of Claim 1 and 13 of the '235 Patent, I have discussed the meaning of amplifying and "co-amplifying" (see paragraphs 32-33, above). I have also noted that the Identifiler® Kit (see paragraphs 55-57) "co-amplifies" to produce a mixture of alleles. With regard to step d) of Claim 1 and 13 of the '235 Patent, I have previously indicated that the Identifiler® Kit (see paragraph 52) is able to "amplify and type" in the context of an ABI PRISM machine and thereby accurately characterize the alleles present (paragraph 62). Therefore, I conclude that the technical elements for steps a) through d) of these claims are found in the accused kit.

137. Claim 4 depends on Claim 1 of the '235 Patent and specifies that the set of loci "further comprises a locus to identify the gender …". The Identifiler® Kit is identified as providing a gender identifying locus (paragraph 58). Therefore, I conclude that the technical elements for Claim 4 are found in the accused kit.

138. Claim 7 depends on Claim 1 and specifies "using pairs of oligonucleotide primers flanking the loci analyzed." As noted previously, the Identifiler® Kit uses primers which flank the repeating sequence. Otherwise they could not amplify the STR loci they claim as referenced above. Therefore, I conclude that the technical elements for Claim 7 are found in the accused kit.

139. Claim 8 depends on Claim 7 and specifies that the set of loci "is co-amplified using a polymerase chain reaction". As noted above, the Identifiler® Kit is provides reagents to co-amplify loci using a "polymerase chain reaction" (paragraphs 52, 55-57). Therefore, I conclude that the technical elements for Claim 8 are found in the accused kit.

140. Claim 9 depends on Claim 7 and specifies that each locus is co-amplified "using a pair of primers which flank the locus wherein at least one primer of each pair has a fluorescent label covalently attached thereto"." As noted above, all of the accused products, including the Identifiler® Kit, use primers which flank the repeating sequence. Otherwise they could not amplify the STR loci they claim as referenced above. Moreover, I have previously noted that the primers are fluorescently labeled (paragraphs 58-59). Therefore, I conclude that the technical elements for Claim 9 are found in the accused kit.

141. Claim 10 depends on Claim 9 and specifies that "at least three" of the labeled primers have different fluorescent labels covalently attached thereto." The Identifiler® Kit is identified as providing that at least three primers are differentially labeled (see paragraphs 58-60). Therefore, I conclude that the technical elements for Claim 10 are found in the accused kit.

142. Claim 12 depends on Claim 1 and specifies that the amplified alleles are evaluated by comparing to "a size standard, wherein the size standard is selected from a group of size standards consisting of a DNA marker and a locus specific allelic ladder. " I have noted previously that the Identifiler® Kit comes with an allelic ladder that is locus specific (paragraphs 61-62) and that a size standard is indicated a "required materials." (paragraph 67).

143. Claim 15 depends on Claim 13 and specifies that the multiplex amplification reaction "is a polymerase chain reaction." As noted above, the Identifiler® Kit provides reagents to co-amplify loci using a "polymerase chain reaction" (paragraphs 52, 55-57). Therefore, I conclude that the technical elements for Claim 15 are found in the accused kit.

144. Claim 16 depends on Claim 13 and specifies that the amplified alleles are evaluated by comparing to a "size standard, wherein the size standard is selected from a group of size standards consisting of a DNA marker and a locus specific allelic ladder." As noted above, the Identifiler® Kit comes with a locus specific allelic ladder (paragraphs 61-62) and that a size standard is indicated as "required materials." (paragraph 67). Therefore, I conclude that the technical elements for Claim 16 are found in the accused kit.

CURRICULUM VITAE

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EDUCATION

1997	Ph.D. Genetics State University of New York (SUNY) at Stony Brook Stony Brook, NY
1979	M.Sc. Forensic Science University of Strathclyde Glasgow, Scotland
1976	B.Sc. (Hons) Biochemistry University of Glasgow Glasgow, Scotland

CURRENT POSITION(S)

2009-present	Professor (tenured) Department of Chemistry University of Central Florida, Orlando, FL
1998-2009	Associate Professor (tenured) Department of Chemistry University of Central Florida, Orlando, FL
2000-present	Assistant Director (Biological Evidence) National Center for Forensic Science, Orlando, FL
2001-present	Associate Director (Research) National Center for Forensic Science, Orlando, FL
2009-present	Professor Biomolecular Science Center University of Central Florida, Orlando, FL

2003-2009 Associate Professor
Biomolecular Science Center
University of Central Florida, Orlando, FL

PREVIOUS EMPLOYMENT

1987-1998 Manager/Supervisor and DNA Technical Manager
Biological Sciences Section, Suffolk County Crime Laboratory, NY

1982-1987 Forensic Biochemist, Hong Kong Government Laboratory, Hong Kong

1979-1982 Forensic Biologist, Strathclyde Police Forensic Science Laboratory, Glasgow, UK

1977-1978 Inspector of Police, Royal Hong Kong Police, Hong Kong

1976-1977 Police Constable, Strathclyde Police, Glasgow, Scotland

CERTIFICATION AND LICENSURES

1993-2003 Diplomate of the American Board of Criminalistics (D-ABC)

1987-1997 Chartered Biologist and a Member of the Institute of Biology (U.K.) (CBiol, MIBiol)

OTHER ACADEMIC APPOINTMENTS

1997 Clinical Assistant Professor of Health Sciences, School of Health Technology and Management, SUNY, Stony Brook, NY (part time and voluntary)

1998 Clinical Associate Professor of Health Sciences, School of Health Technology and Management, SUNY, Stony Brook, NY (part time and voluntary)

HONORS

1976 Honors Degree in Biochemistry (B.Sc.) (University of Glasgow, U.K.)

1976 PMAS Book Prize and 7/70 Trophy, Scottish Police College

1979 Forensic Science Society Book Prize for the most meritorious student attending the M.Sc. Forensic Science program at Strathclyde University

1999 Directorate Merit Award for assistance given to Royal Canadian Mounted Police in connection with the Swissair 111 Aircraft disaster

1999	Commemoration award from the FBI for service to the FBI and forensic community as a member of the DNA Advisory Board
2002	Certificate of Appreciation from the Director, National Institute of Justice "for outstanding contributions as a member of the Kinship and Data Analysis Panel in support of the World Trade Center DNA effort"
2004	Received a Research Incentive Award (RIA) from the University of Central Florida in recognition of outstanding research accomplishments
2006	Inducted into the UCF Millionaires Club (for faculty members who have brought at least $1 million in external research funds into the University)
2008	Awarded an ESR (Institute of Environmental Science and Research), New Zealand, International Fellowship
2009	Received a Research Incentive Award (RIA) from the University of Central Florida in recognition of outstanding research accomplishments

SCIENTIFIC SOCIETY MEMBERSHIP

- American Academy of Forensic Sciences (AAFS)
- American Association for the Advancement of Science (AAAS)
- American Chemical Society (ACS)
- International Society of Forensic Genetics (ISFG)

CONSULTING ACTIVITIES

1998-2000	DNA Technical Leader (Consultant) for the Mississippi Crime Laboratory, Jackson, Mississippi
1998-2000	DNA Technical Leader (Consultant) for the State of Delaware Office of Chief Medical Examiner, Wilmington, Delaware
1999-2000	DNA Technical Leader (Consultant) for the South Western Institute for Forensic Science (SWIFS), Dallas County, Texas
2001-2002	Technical Leader (Consultant) for the Sedgwick County Regional Forensic Science Center, Wichita, Kansas

- National Forensic Science Technology Center, St. Petersburg, FL
- US Department of Energy, Washington DC
- Lakehead University, Ontario, Canada
- Onondaga County, NY
- Standards Council for Canada
- Lockheed Martin

CONTINUING EDUCATION / ADDITIONAL TRAINING

1988	Graduate credits in Analytical Separations (3cr. A) from the City University of New York (CUNY)
1989	DNA-Forensic Applications, University of New Haven, CT
1988-1989	Training in the use of molecular biology techniques in the laboratory of Dr. Paul Bingham, Dept. of Biochemistry, SUNY Stony Brook, NY
1989-1979	Training in the use of molecular biology techniques in the laboratory of Dr. Ken Marcu, Dept of Biochemistry, SUNY, Stony Brook, NY
1989	Forensic Application of DNA Typing Methods, FBI Academy, Quantico, VA (Graduate credits in Laboratory Applications of DNA (3cr. A) and Forensic Applications of DNA (3cr. A) from the University of Virginia, VA)
1992	Advanced DNA Typing School at the FBI, Forensic Science Research and Training Center, Quantico, VA.
1994	Statistical Methods in Forensic DNA Analysis, NEAFS Annual Meeting New York, NY
1995	Implementation and Consequences of New DNA Technologies: the Sequel, American Academy of Forensic Sciences, Seattle, WA
1995	Advanced PCR Applications, Florida Crime Laboratory Council and the Florida Forensic Advisory Committee, Orlando, FL
1995	Workshop in Statistics for Forensic Scientists, National Forensic Science Technology Center, St. Petersburg, FL
1995	Advanced DNA Technologies Workshop, American Academy of Forensic Sciences, Nashville, TN
1995	DNA Databanks and Repositories and CODIS Users Group Meeting, Tallahassee, FL (Armed Forces Institute of Pathology)

1995	Advanced DNA Technologies: Automation and Application, American Academy of Forensic Sciences, New York City, NY (invited speaker)
1997	Forensic Sciences Summit: Roadmap to the Year 2000. NIJ/NIST(OLES)/ASCLD workshop, Gaithersburg, MD. Workshop proceedings published by NIJ (1999) (Forensic Sciences: Review of Status and Needs)
1997	Presenting DNA Statistics in Court, Promega 8th International Symposium on Human Identification, Scottsdale, AZ.
1997	Statistics Training for DNA Scientists. Division of Criminal Justice Services, Albany, NY. Two day workshop conducted by Bruce Weir, North Carolina State University
1997	Florida DNA Training Session IV: STRs-The Next Generation. Florida Crime Laboratory Council and the Florida Forensic Advisory Committee, Orlando, FL
2000	ISO/IEC 17025 Assessor Training, Laboratory Accreditation Bureau
2001	SWGDAM, FBI Academy, Quantico, VA
2002	SWGDAM, FBI Academy, Quantico, VA
2003	SWGDAM, FBI Academy, Quantico, VA
2003	Low Copy Number DNA and Extracting DNA Profiles from Challenging Sample Materials Workshops, AAFS, Chicago
2004	Forensic Human Mitochondrial DNA Analysis, AAFS Annual Meeting, Dallas, TX
2004	Y-STR Analysis on Forensic Casework, AAFS Annual Meeting, Dallas, TX
2004	Applied Biosystems Annual User Forum, AAFS Annual Meeting, Dallas, TX
2004	SWGDAM, FBI Academy, Quantico, VA
2005	SWGDAM, FBI Academy, Quantico, VA
2006	SWGDAM, FBI Academy, Quantico, VA
2007	SWGDAM, FBI Academy, Quantico, VA
2007	Statistical Analysis of Real-time PCR Data, CHI Quantitative PCR Conference, San Diego, CA
2008	SWGDAM, FBI Academy, Quantico, VA

PRESENTATIONS

1984 The ABO Typing of Hair as a Routine Casework Method. International Association of Forensic Sciences, Oxford, UK

1988 Quality Assurance in the Forensic Serology Laboratory. Northeastern Association of Forensic Scientists Annual Meeting, Mystic, CT

1992 Validation of AHSG as a Genetic Marker System in Forensic Science. Co-author with L.S. Remmert. Northeastern Association of Forensic Scientists Annual Meeting, Atlantic City, NJ.

1992 Extraction Strategies for Routine HLA DQα Analysis. Co-author with R.S. Jordan and L.S. Remmert. Northeastern Association of Forensic Scientists Annual Meeting, Atlantic City, NJ

1993 Use of a Semi-Automated Multiplex PCR Method to Evaluate Four Short Tandem Repeat Loci. Co-author with J.B. Sgueglia, A. Juston and J. Galdi. Northeastern Association of Forensic Scientists Annual Meeting, Springfield, MA

1994 Validation Studies on a Semi-Automated Multiplex Analysis of Four Short Tandem Repeat Loci, HUMVWA31, HUMTH01, HUMF13A1 and HUMFES/FPS. Co-author with J.B. Sgueglia, A. Juston and K. Galindo. Northeastern Association of Forensic Scientists (NEAFS) Annual Meeting, New York, NY

1994 The Efficacy of PM Analysis for Routine Forensic Biology Casework. Co-author with L. S-Reich and R. S. Jordan. NEAFS Annual Meeting, New York, NY

1994 A Sensitive Rapid Gender Identification Test Utilizing the X-Y Homologous Gene Amelogenin. Co-author with K. Galindo. NEAFS Annual Meeting, New York, NY

1994 Trace and DNA: A Hairy Experience. Co-author with J.B. Sgueglia, T. Zaveski, and L.S-Reich. NEAFS Annual Meeting, New York, NY

1994 Revising an Existing PGM ULPAGIF Method to Accommodate Pharmacia's Reformulated Ampholines. Co-author with C. Wagner, A. Juston, P. Dhawan, R. Baumann and D. Alia. NEAFS Annual meeting, New York, NY

1995 The Integration of HLA DQα and PM Analysis into an Operational Forensic Biology Setting. Amplitype Users Forum, AAFS, Seattle, WA

1995 The Evaluation of Chemiluminescent RFLP Probes for Forensic Casework. Co-author with J.B. Sgueglia, M. Philip and T.L. Ferguson. NEAFS Annual Meeting, Mystic, CT

1995 The Long Island Fingernail Phenomenon. Co-author with D. Alia, R.S. Jordan

and L.S. Reich. NEAFS Annual Meeting, Mystic, CT

1995 Use of Bovine Serum Albumin (BSA) as a PCR Additive. Co-author with R. S. Jordan, J. Eberhardt, and L.S. Reich. NEAFS Annual Meeting, Mystic, CT

1996 Multiple STR Multiplexes Make for a Multitude of Possible Genotypes. Amplitype Users Forum, AAFS, Nashville, TN

1996 Quality Assurance in the DNA Laboratory. National Conference on the Future of DNA: Implications for the Criminal Justice System. Washington, DC

1996 Forensic Casework Analysis Using Multiple STR Multiplexes on a Multitude of Sample Types. Co-author with Sgueglia, J.B. and Juston, A.C. Seventh International Symposium on Human Identification. Scottsdale, AZ

1996 Forensic Casework Analysis Using Multiple STR Multiplexes on a Multitude of Sample Types. Co-author with Sgueglia, J.B.S. and Juston, A.C. NEAFS Annual Meeting, Poconos, PA

1996 TWA Mass Disaster-Identification of Human Remains. Co-author with Sgueglia, J.B., Juston, A.C., Reich, L.S., Jordan, R.S., Galdi, J. And Phillip, M. NEAFS Annual Meeting, Poconos, PA

1996 DNA Advisory Board, Eastern Analytical Symposium, Somerset, NJ

1997 TWA Flight 800 Mass Disaster-DNA Identification of Human Remains. Co-author with Sgueglia, J.B., Juston, A.C., Sherlock-Reich, L., Scioli-Jordan, R., Galdi, J. and Philip, M. AAFS Annual Meeting, New York, NY

1997 Multiple STR Multiplexes Make for a Multitude of Possible Genotypes. Co-author with Sgueglia, J.B. and Juston, A. AAFS Annual Meeting, New York, NY

1997 Validation and Casework Analysis Using a Megaplex STR System. Co-author with Sgueglia, J.B., Juston, A.C., Dooling, K.E. and Cannella, C. NEAFS Annual Meeting, White Plains, NY

1998 Casework Analysis Using a Megaplex STR System for Human Identification. Co-author with Sgueglia, J.B., Juston, A.C., Dooling, K.E., Sherlock-Reich, L., Scioli-Jordan, R. and Willard, J. M. AAFS Annual Meeting, San Francisco, CA

1998 The Use of DNA Analysis to Identify Victims of Mass Disasters: TWA Flight 800 and the Wyman-Gordon Forgings, Inc., Explosion. Co-author with Willard, J.M., Lee, D.A., Ross, J.P., Wilson, R.E. and Holland, M.M. AAFS Annual Meeting, San Francisco, CA

1998 Electrophoretic variation at the FGA Locus. Co-author with Sgueglia, J.B.,

Juston, A.C. and Essex,B. NEAFS Annual Meeting, Rhode Island

1998 Testing, Evaluation and Validation, CLIP Summit, NIJ, Washington, DC

2000 How Can DNA Research and Development Enhance Victim's Rights? The Fifth Annual Conference on the future of DNA: Implications for the Criminal Justice System. The National Institute of Justice, U.S. Department of Justice. New York, New York

2001 Development of a Panel of Y Chromosome Markers for Forensic Use. Co-author with Hall, A. AAFS Annual Meeting, Seattle, WA

2001 The Development of a panel of Y chromosome Markers for Forensic Use. Center for Bioinformatics, North Carolina State University, Raleigh-Durham

2001 The Development of an RNA Based Assay System To Supplant Conventional Methods for Body Fluid Identification. Co-author with Juusola, J. 12th International Symposium on Human Identification, Biloxi, MS

2001 The Role of the Crime Laboratory in Mass Fatality Incidents. American Society of Crime Laboratory Directors (ASCLD) Annual Meeting, Phoenix, AZ

2001 Forensic Identification by Nuclear and Mitochondrial DNA. Maples Center for Forensic medicine, University of Florida, Gainsville, FL

2002 Robust Multiplex Amplification of Y-STR Loci. Co-author with Hall, A. AAFS Annual Meeting, Atlanta, GA

2002 New ways of looking at old and old ways of looking at new DNA. Ancient DNA Training Program, Lakehead University, Thunder Bay, Canada

2002 The Development of an RNA Based Assay System for Body Fluid Stain Identification. Co-author with Juusola, J. AAFS Annual Meeting, Atlanta, GA

2002 Forensic Biometrics: The Determination of Individual Physical Characteristics by DNA Typing. Co-author with Kotkin, M. 13th International Symposium on Human Identification, Phoenix, AZ

2002 Body Fluid Identification by RNA Profiling. Future Directions in Forensic Biology Workshop. SWAFS 2002 Training Conference, Scottsdale, AZ

2002 Y-Chromosome Markers. Future Directions in Forensic Biology Workshop. SWAFS 2002 Training Conference, Scottsdale, AZ

2002 Assessment and Repair of Damaged DNA. Future Directions in Forensic Biology Workshop. SWAFS 2002 Training Conference, Scottsdale, AZ

2003 Highly Discriminating Y-STR Multiplexes Suitable for Forensic Use to Permit the Determination of 49-loci Male Haplotypes. Co-author with Hansen, E. AAFS Annual Meeting, Chicago, IL

2003 DNA Identification of Mass Fatality Casualties. Florida Emergency Mortuary Response System Training Seminar, Orlando, FL

2003 A Mass Fatality Guide for Medical Examiners and Coroners. Co-author with Whitcomb, C. AAFS Annual Meeting, Chicago, IL

2003 The Design and Compilation of a US Y -STR Haplotype Reference Database. Co-author with Berdos, P., and Hansen, E. AAFS Annual Meeting, Chicago, IL

2003 Y-SNP Analysis by Pyrosequencing. Co-author with Fletcher, J. AAFS Annual Meeting, Chicago, IL

2003 Strategies for Typing DNA from Damaged Spermatozoa. Co-author with Hall, A. Extracting DNA Profiles from Challenging Sample Materials Workshop. AAFS Annual Meeting, Chicago, IL

2003 Innovative Uses of Y Chromosome Markers in Forensic Science. Ancient DNA Training Program, Lakehead University, Thunder Bay, Canada

2003 Assessment of Damaged DNA Templates. Co-author with Hall, A. NIJ fourth Annual DNA Grantees Workshop, Washington DC

2003 Streamlined Processing of Sexual Assault Kits: Programs and Early Applications. Co-author with Hall, A. NIJ fourth Annual DNA Grantees Workshop, Washington DC

2003 DNA Profiling of the Semen Donor in Extended Interval ($\geq$48 h) Post Coital Cervicovaginal Samples. Co-author with Hall, A. European Academy of Forensic Sciences of the European Forensic Science Institutes, Istanbul, Turkey

2003 Messenger RNA Profiling for Body Fluid Identification. Co-author with Juusola, J. FBI Symposium on Crime Laboratory Management. Minneapolis, MN

2004 Stability and Recovery of mRNA in Biological Stains. Co-author with Setzer, M. and Juusola, J. AAFS Annual Meeting, Dallas, TX

2004 mRNA Profiling: Body Fluid Identification Using Multiplex RT-PCR. Co-author with Juusola, J. and Miller, K. AAFS Annual Meeting, Dallas, TX

2004 Strategies for Low Copy Number (LCN) DNA Analysis. Co-author with Hanson, E. and Raker, V. AAFS Annual Meeting, Dallas, TX

2004 Mitochondrial DNA Analysis by Pyrosequencing. Co-author with Hastings, S. and Dugan, K. AAFS Annual Meeting, Dallas, TX

2004 The Design and Development of a Comprehensive 49 Locus Y-STR Database For Major U.S. Populations (poster). Co-author with Berdos, P. AAFS Annual Meeting, Dallas, TX

2004 The Design and Development of a Comprehensive 49 Locus Y-STR Database For Major U.S. Populations. Co-author with Berdos, P. Y-STR Analysis on Forensic Casework Workshop, AAFS Annual Meeting, Dallas, TX

2004 Getting Blood Out of Stone: Eking Out More Information from Physiological Stains. Applied Biosystems Annual Users Forum, AAFS Annual Meeting, Dallas, TX

2004 Assessment and *In Vitro* Repair of Damaged DNA Templates. Co-author with Hall, A. Florida Academy of Sciences Annual Meeting, Orlando, FL

2004 mRNA Profiling: Body Fluid Identification Using Multiplex RT-PCR. Co-author with Juusola, J. Florida Academy of Sciences Annual Meeting, Orlando, FL

2004 mRNA Profiling: Body Fluid Identification Using Multiplex RT-PCR. Mid West Association of Forensic Scientists (MAFS) Spring Workshop, Chicago, IL

2004 Pyrosequencing Applications in Forensic Science: Y-SNPs, mtDNA Analysis and Microbial Forensics. Mid West Association of Forensic Scientists (MAFS) Spring Workshop, Chicago, IL

2004 mRNA Profiling: Body Fluid Identification Using Multiplex RT-PCR. Ancient DNA Internship Program, Paleo-DNA Laboratory, Lakehead University, Thunder Bay, Ontario, Canada

2004 The Molecular Genetics of the Y Chromosome and the Utility of Y-Chromosome Markers in Forensic Science. Forensic DNA Technology Workshop, Promega Corporation and Center for Forensic Sciences, Toronto, Canada

2004 Assessment and Repair of Damaged DNA Templates. Co-author with Hall, A. NIJ Fifth Annual DNA Grantees Workshop, Washington DC

2004 Determination of the Age of an Individual from Biological Samples Deposited at the Crime Scene. Annual Conference on Criminal Justice Research and Evaluation, Washington DC

2004 Assessment and Repair of Damaged DNA Templates. Co-author with Hall, A. Joint Meeting of the Canadian Society of Forensic Scientists, MAFS, MWAFS and SAFS, Orlando, FL

2004 A Modified Whole Genome Amplification Method for STR Analysis Using Single or Few Cell Equivalents of Input genomic DNA. Co-author with Hanson, E. Joint Meeting of the Canadian Society of Forensic Scientists, MAFS, MWAFS and SAFS, Orlando, FL

2004 Age Determination: The Identification of Newborns Using messenger RNA Profiling Analysis. Co-author with Alvarez, M. Joint Meeting of the Canadian Society of Forensic Scientists, MAFS, MWAFS and SAFS, Orlando, FL

2004 mRNA Profiling: Body Fluid Identification Using Multiplex Real Time PCR. Co-author with Juusola, J. Joint Meeting of the Canadian Society of Forensic Scientists, MAFS, MWAFS and SAFS, Orlando, FL

2004 The Forensic Biology Program at the National Center for Forensic Science. The FRN/CLIP National Conference: Innovative Partnerships. Tampa, FL

2004 Principles of Nucleic Acid Biochemstry. Fundamentals of Molecular Biology for Forensic Scientists Workshop. 15th International Symposium on Human Identification, Phoenix, AZ

2004 Y chromosome Biology. Fundamentals of Molecular Biology for Forensic Scientists Workshop. 15th International Symposium on Human Identification, Phoenix, AZ

2004 Basic Population Genetics. Fundamentals of Molecular Biology for Forensic Scientists Workshop. 15th International Symposium on Human Identification, Phoenix, AZ

2004 Inference of Human Geographic Origins Using *ALU* Insertion Polymorphisms. Co-author with Ray, D., Walker, J., Hall, A., Llewellyn, B., Christian, A., Turteltaub, K. and Batzer, M. 15th International Symposium on Human Identification, Phoenix, AZ

2004 Assessment and *In Vitro* Repair of Damaged DNA Templates-Forensic Implications. Co-author with Hall, A. American Society for Microbiology Conference. DNA Repair and Mutagenesis: From Molecular Structure to Biological Consequences, Southampton, Bermuda

2005 A Lot from a Little: Forensic Genetics at UCF/NCFS. Midwest Research Institute (MRI), Palm Bay, FL

2005 Strategies for the Automation of Forensic Serology Operations. Quest for Automation and the Reality of Quality Standards Workshop. Sponsored by Fitzco Inc. and Quality Forensics. AAFS Annual Meeting, New Orleans.

2005 Age Determination: The Identification of Newborns Using Messenger RNA Profiling Analysis. Co-author with Alvarez, M. AAFS Annual Meeting, New Orleans

2005 Assessment and *In Vitro* Repair of Damaged DNA Templates. Co-author with Hall, A. AAFS Annual Meeting, New Orleans

2005 mRNA Profiling for Body Fluid Identification Using Multiplex Real-Time PCR. Co-author with Juusola, J. AAFS Annual Meeting, New Orleans

2005 mRNA Profiling: Body Fluid Identification Using Multiplex Real-Time PCR. Co-author with Juusola, J. Promega's 16th International Symposium on Human Identification, Grapevine, TX

2005 The Future of DNA Profiling in Sexual Assault Investigations. Keynote speech. International Symposium on Sex Crimes, Toronto Police Department, Toronto, Canada

2005 Future of DNA Including Strategies for the Automation of Forensic Serology Operations. External Lecture Series. Centre for Forensic Sciences, Toronto, Canada.

2005 DNA-STR Testing in Criminal Investigations and Mass Disasters. Department of Anthropolgy, University of Western Ontario, Canada

2005 An investigation of YSTR haplotype clustering among 298 Caucasian men in the US. American Society of Human Genetics Annual Meeting, Salt Lake City Utah. Co-author with Garvey, D., Berdos, P. and Sims, L.

2005 mRNA Applications in Forensic Genetics. Applied Biosystems Seminars, Foster City, CA

2006 The Biological Evidence Program at the National Center for Forensic Science, NIJ Applied Technologies and Partnerships Conference, Hilton Head, SC

2006 Age Identification by RNA Profiling: Validation of a Newborn Child- Specific Real-Time PCR Assay. Co-author with Alvarez, M. AAFS Annual Meeting, Seattle, WA

2006 Biochemical Repair and Lesion Bypass of Damaged DNA. Co-author with Hall, A, Woodgate, R and McDonald, J.AAFS Annual Meeting, Seattle, WA

2006 mRNA Profiling: Identification of Solid Tissues of Forensic Interest by Multiplex Real-Time PCR. Co-author with Juusola, J. AAFS Annual Meeting, Seattle, WA

2006 Development of a Speedy Rape Kit Screening Method. Co-author with Hall, A. AAFS Annual Meeting, Seattle, WA

2006 A Comparison of the Performance of Commercial Y-STR Kits for Operational Use with Challenging Samples: Extended Interval Post-Coital Samples, Mixtures and Environmental Insults Co-author with Press, K. and Hall, A. AAFS Annual Meeting, Seattle, WA

2006 Population genetics of the Y chromosome and application of Y-STRs to casework. Future Trends in Forensic DNA Technology, Practical STR Statistics Workshop, Los Angeles, CA.

2006 mRNA Tissue Identification. The Bode Technology Group Third Annual Advanced DNA Technology Workshop, San Diego, CA.

2006 Ethnogeographic Profiling: The Development of a Hierarchical SNP Typing System to Predict Ethnogeographic Ancestry. Co-author with Sims, L. and Garvey, D. Forensic Sciences Symposium, Nova Southeastern University, Ft. Lauderdale, FL

2006 Taught Degree Courses: US Experience. International Forensic e-Symposium™ on Forensic Education, The Forensic Institute 2006 Series (www.e-symposium .com)

2006 The Compilation and Management of a Comprehensive US Y-STR Reference Database. Co-author with Fatolitis, L. Annual NIJ DNA Grantees Meeting, Washington DC

2006 The Determination of the Physical Characteristics of an Individual fromBiological Stains: Age Determination. Co-author with Alvarez, M. Annual NIJ DNA Grantees Meeting, Washington DC

2006 Human Identity Testing: A Biotechnology Based Revolution. Qiagen Investor and Analyst Meeting, New York City

2006 Mass Fatality Incident Management. Technologies for Critical Incident Preparedness Conference and Exposition. Atlanta, GA

2006 Burnett Honors College's Career Opportunities in the Biomedical Sciences. Forensic Science Careers. University of Central Florida, Orlando, FL

2006 The Use of Recently Phylogenetically Defined Y-SNPs in a Typing System to Predict Ethnogeographic Ancestry Using Pyrosequencing Technology. Sims, L., Garvey D. and Ballantyne, J. 17th International Symposium on Human Identification, Nashville, TX

2006 Strategies for Obtaining a DNA Profile of the Male Donor in Extended Interval (>72h) Post-Coital Cervico-Vaginal Samples Using Commercial Y-STR Multiplex Systems: Extraction Techniques, Post Amplification Clean Up and Novel Enzymes. Mayntz-Press, K. and Ballantyne, J. 17th International Symposium on Human Identification, Nashville, TX

2006 Dual Extraction of RNA and DNA from Human Body Fluids for Use in Forensic Casework. Hall, K., Kelly, A., Lin, M., Ballantyne, J., Craig, R. and Dugan, K. 17th International Symposium on Human Identification, Nashville, TX

2006 The SWGDAM Y Committee and the Consolidated National Y-STR Database. National CODIS Meeting, Crystal City, VA

2006 The Determination of Physical Features of the Donor of a Crime Scene Sample. National Conference on Science and the Law. St Petersburg, FL.

2007 The Differentiation of Sub-Populations within Y-SNP Haplogroup G. Sims, L., Klega, K., Garvey, D. and Ballantyne, J. Forensic Sciences Symposium, Nova Southeastern University, Ft. Lauderdale, FL.

2007 Microbial Genetic Signatures. Donigan, M. and Ballantyne, J. Forensic Sciences Symposium, Nova Southeastern University, Ft. Lauderdale, FL.

2007 Biochemistry of Dry State DNA: Comparison of Depurination Rates of Bases. Pope, A. and Ballantyne, J. Forensic Sciences Symposium, Nova Southeastern University, Ft. Lauderdale, FL.

2007 The Development of a Highly Informative, Hierarchical Multiplex SNP Typing System to Predict Ethnogeographic Ancestry Using Pyrosequencing Technology. Sims, LM, Garvey, D and Ballantyne, J. AAFS Annual Meeting, San Antonio, TX

2007 Simplified Low Copy Number (LCN) DNA Analysis by Post PCR Purification. Smith, PJ and Ballantyne, J. AAFS Annual Meeting, San Antonio, TX

2007 Novel Techniques for Identifying the Semen Donor in Extended Interval Post-Coital Samples. Mayntz-Press, K, Sims, L and Ballantyne, J. AAFS Annual Meeting, San Antonio, TX

2007 The Forensic Identification of Newborns using Messenger RNA Profiling Analysis. Alvarez, M. and Ballantyne, J. Cambridge Healthtech International Meeting on Quantitative PCR, San Diego, CA

2007 Alternative Strategies to Increased Cycle Number for Low Copy Number (LCN) DNA Analysis. Forensic e-SymposiumTM. Human Identification: Profiling of

degraded and low amounts of DNA

2007 The Determination of the Physical Features of the Donor of a Crime Scene Sample. NIJ Applied Technology Conference, Orange County, CA.

2007 Getting Blood form a Rock: Getting More and More from Less and Less. International Society for Optical Engineering (SPIE) Defense and Security Symposium, Orlando, FL

2007 Y-STR Profiling in Extended Interval (> 3 days) Post Coital Samples. Future Trends in Forensic DNA Technology Seminar Series (Applied Biosystems HID University), Chicago, IL.

2007 Double Strand Break Repair of Damaged DNA Templates. Lamers, R and Ballantyne, J. The NIJ Conference. Arlington, VA

2007 Forensic Resource Network Operational Casework Support Programs at the National Center for Forensic Science. The NIJ Conference. Arlington, VA

2007 A Genetic Eyewitness: The Determination of Physical Characteristics of the Donor of a Body Fluid Stain. The NIJ Conference. Arlington, VA

2007 Determination of the Age (Time Since Deposition) of a Biological Stain. Hanson, E. and Ballantyne, J. The NIJ Conference. Arlington, VA

2007 The Determination of the Physical Characteristics of an Individual from Bloodstains: Biological Age Determination. Alvarez, M. and Ballantyne, J. The NIJ Conference. Arlington, VA

2007 Y-STR Profiling in Extended Interval (> 3 days) Post Coital Samples. Future Trends in Forensic DNA Technology Seminar Series (Applied Biosystems HID University), Waltham, MA.

2007 Y-STR Operational Casework Support Programs at the National center for Forensic Science. Association of Forensic DNA Analysts and Administrators summer meeting, Austin, TX

2007 Long Term Ambient Temperature Storage, Stability, and Recovery Efficiency of RNA from a Reversible Porous Nanoparticle Matrix. Alvarez, M., Almazan, M., Hogan, M., Utermohlen, J. and Ballantyne, J. 18th International Symposium on Human Identification, Hollywood, CA

2007 Repair of Human DNA from Forensic Samples. Loseke, D., Carrano, J., Ballantyne, J., McDonald, J., Woodgate, R. and Hall, A. 18th International Symposium on Human Identification, Hollywood, CA

2007 Determining the Physical Characteristics of an Individual from Bloodstains: Biological Age Determination. Alvarez, M. and Ballantyne, J. 18th International Symposium on Human Identification, Hollywood, CA

2007 The Whys and Whatnots of Y-STR Casework Analysis. General Electric Global Research and the University of Albany Northeast Regional Forensic Institute, Forensic DNA Initiatives Seminar, Niskayuna, NY

2007 Biology of the Y Chromosome and Y-STRs. New technologies and applications in forensic biology workshop. 2nd Tri-Division Educational Conference. Utah Division, Nevada State Division and the Arizona Identification Council of the International Association for Identification in conjunction with the Northwest Association of Forensic Scientists. Salt Lake City, UT.

2007 Getting Blood from a Stone: Getting More and More Forensic Evidence form Less and Less. Qiagen Corporation, Gaithersburg, MD.

2008 Incarcerations and Exonerations: The Key Role of the Forensic Sciences. Incarcerations and Exonerations-Criminalistics (DNA). AAFS Annual Meeting, Washington, DC.

2008 DNA Profiling of the Semen Donor in Extended Interval (> 72 h) Post Coital Cervicovaginal Samples. Ballantyne, J. and Hanson, E. NIJ Applied Technologies Conference, Point Clear, AL.

2008 Its 2008, what can the Crime Lab do for you: New Technologies and DNA? Ballantyne, J. and Hanson, E. NIJ Applied Technologies Conference, Point Clear, AL.

2008 Not your CSI DNA Profiling: Messenger RNA Profiling Applications in Bio-Molecular Forensics. Department of Chemistry Seminar Series, Florida International University, Miami, FL.

2008 Biology of the Y Chromosome and Y-STRs. New Technologies and Applications in Forensic Biology Workshop, New Jersey State Police, Hamilton, NJ.

2008 Messenger RNA Profiling: A Prototype Method for Body Fluid and Tissue Identification. New Technologies and Applications in Forensic Biology Workshop, New Jersey State Police, Hamilton, NJ.

2008 Messenger RNA Profiling: Prediction of the Age of an Individual from RNA Recovered from the Crime Scene. New Technologies and Applications in Forensic Biology Workshop, New Jersey State Police, Hamilton, NJ.

2008 A 'Genetic Eyewitness': the Determination of the Physical Features of the Donor of a Crime Scene Sample. New Technologies and Applications in Forensic

Biology Workshop, New Jersey State Police, Hamilton, NJ.

2008 Data Preparation for Forensic DNA Typing. Johnson, M. and Ballantyne, J. Discovery 2008 (the data exploration conference), Cary, NC.

2008 Double Strand Break Repair of Damaged DNA Templates. Ballantyne J. and Lamers, R. The NIJ Conference, Crystal City, VA.

2008 Hypsochromic Spectral Shifts of the Hemoglobin Soret Band Correlate with the Time since Deposition of Dried Bloodstains. Hanson, E. and Ballantyne J. The NIJ Conference, Crystal City, VA.

2008 Improved Detection of Male DNA from Post-Coital Samples. Ballantyne J. and Hanson, E. The NIJ Conference, Crystal City, VA.

2008 DNA Profiling of the Semen Donor in Extended Interval Post-Coital Samples Ballantyne J. and Hanson, E. The NIJ Conference, Crystal City, VA.

2008 Y-STR Databases. Webinar, California Criminalistics Institute, Jan Bashinski DNA Laborarory, Richmond, CA.

2008 Y-STR Interpretation Guidelines. Webinar, California Criminalistics Institute, Jan Bashinski DNA Laborarory, Richmond, CA.

2008 New Y-STR Multiplexes. Webinar, California Criminalistics Institute, Jan Bashinski DNA Laborarory, Richmond, CA.

2008 A Y-STR Mixture Frequency Estimator. Macmillan, K., Gefrides, L., Klein, C., Fatolitis, L., Ballantyne, J. and Kahn, R. 19th International Symposium on Human Identification, Hollywood, CA.

2008 Hypsochromic Spectral Shifts of the Hemoglobin Soret Band Correlate with the Time since Deposition (TSD) of Dried Bloodstains. Hanson, E. and Ballantyne, J. 19th International Symposium on Human Identification. Hollywood, CA.

2008 The Fundamental Biochemistry of Dry State DNA: Hydrolytic Reactions. Marrone, A. and Ballantyne, J. 19th International Symposium on Human Identification, Hollywood, CA.

2008 Research at the National Center for Forensic Science. ESR Forensic Group, Auckland, New Zealand.

2008 Research at the National Center for Forensic Science. ESR Headquarters, Wellington, New Zealand.

2008 Why the Y?: Y Chromosome Biomarker Applications in Sexual Assault

Investigations. New Zealand Forensic Science Society, Auckland, New Zealand.

2008 Messenger RNA Profiling Applications in Bio-Molecular Forensics. Forensic Science Institute, University of Central Oklahoma, Edmond, OK.

2008 Y Chromosome Applications in Forensic Casework. Arizona Department of Public Safety, Phoenix, AZ

2008 Forensic Biology Research at the National Center for Forensic Science. The 20th EDNAP (European DNA Profiling Group) Meeting, Zurich, Switzerland (NR/I/I)

2008 Messenger RNA Profiling for Body Fluid Identification. The 29th ENFSI (European National Forensic Science Institutes) DNA Working Group Meeting, Zurich, Switzerland (NR/I/I)

2009 Determination of the Age (Time since Deposition) of a Biological Stain. Ballantyne, J. and Hanson, E. BrightTALK DNA Identification Summit. Webinar

2009 A Y-STR Mixture Frequency Estimator in Forensic Casework. MacMillan, K., Genfrides, L., Klein, C., Fatolitis, L., Ballantyne, J. and Kahn, R. AAFS Annual Meeting, Denver, CO.

2009 Post Coital Interval for DNA Testing. The Fifth National SART (Sexual Assault Response Team) Training Conference, Seattle, WA.

2009 Beyond Traditional DNA Markers: Predicting a Person's Appearance from DNA Evidence. The Annual NIJ Conference, Washington, DC.

2009 Sexual Assault: Obtaining DNA from Evidence Collected up to a Week Later. The Annual NIJ Conference, Washington, DC.

2009 De-Convolution of Body Fluid Mixtures: Cell Type Identification and Single Source Genetic Profiling of Micro-Dissected Cells. Ballantyne, J and Hanson, E. The Annual NIJ Conference, Washington, DC.

2009 Improved Detection of Male DNA From Post Coital Samples. Hanson, E., Korfhage, C., Loeffert, D and Ballantyne, J. The Annual NIJ Conference, Washington, DC.

2009 Rapid STR Prescreening of Forensic Samples at the Crime Scene. Halpern, M.D., Gerdes, J.C., Ballantyne, J., Haab, J., Hanson, E. and Kiavand, A. The Annual NIJ Conference, Washington, DC.

2009 Identification of Forensically Relevant Body Fluids Using a Panel of Differentially Expressed microRNAs. Hanson, E., Lubenow, H and Ballantyne, J.

23rd World Congress, International Society for Forensic Genetics, Buenos Aires, Argentina

2009 Body Fluid Identification by RNA Expression Profiling. BrightTALK Forensic Science Community webcast

2009 Rapid STR Prescreening of Forensic Samples at the Crime Scene. Halpern, M.D., Gerdes, J.C., Ballantyne, J., Haab, J., Hanson, E. and Kiavand, A. 20th International Symposium on Human Identification. Promega, Las Vegas, NV

2009 Identification of Forensically Relevant Body Fluids Using a Panel of Differentially Expressed microRNAs. Hanson, E. and Ballantyne, J. 20th International Symposium on Human Identification. Promega, Las Vegas, NV.

2009 Simultaneous Determination of the Time Since Deposition and Identification of Dried Bloodstains Using a Portable Spectrophotometer. Hanson, E. and Ballantyne, J. European National Forensic Science Institutes (ENFSI) DNA Working Group, Edinburgh, UK.

2009 Optimization of Isolation Strategies for the Simultaneous Recovery of DNA and RNA from Forensic Samples. Parker, C, Hanson, E. and Ballantyne, J. Joint Forensic Science Association Meeting (Southern Association of Forensic Science, Mid-Atlantic Association of Forensic Science, Midwestern Association of Forensic Science, Southwest Association of Forensic Science). Orlando, FL.

2009 Recent Research into Extending the Post Coital Time Interval for DNA Profile Recovery. Ballantyne, J. International Association of Forensic Nurses, Sexual Assault Forensic Examiner Technical Assistance (SAFEta) webinar on Timing Considerations for Sexual Assault Examination.

2010 Extending the Post Coital Time Interval for DNA Profile Recovery. Orange County SART (Sexual Assault Response Team), Orlando, FL

2010 MicroRNA Expression Profiling for the Identification of Forensically Relevant Biological Fluids. Cambridge Healthtech Institute's 17th International Molecular Medicine Tri-Conference, San Francisco, CA.

2010 Forensic Biology Research at the National Center for Forensic Science. EDNAP (European DNA Profiling Group) Meeting, The Hague, Netherlands

2010 New York City Frye Hearing 2008-2010 People v. Megnath. The 32nd ENFSI (European National Forensic Science Institutes) DNA Working Group Meeting, The Hague, Netherlands

2010 Not your CSI DNA Profiling: RNA Applications in Forensic Genetics. 12th annual Ancient DNA Training Program, Lakehead University Paleo-DNA

Laboratory, Thunder Bay, Ontario, Canada

2010 Rapid STR Prescreening of Forensic Samples at the Crime Scene. Halpern, M.D., Gerdes, J.C., Ballantyne, J., Haab, J., Hanson, E. and Kiavand, A. The Annual NIJ Conference, Washington, DC.

2010 Identification of Forensically Relevant Body Fluids and Tissues by Small RNA Profiling. Hanson, E. and Ballantyne, J. The Annual NIJ Conference, Washington, DC.

2010 Body Fluid Identification by RNA Profiling. Webinar, California Criminalistics Institute, Jan Bashinski DNA Laborarory, Richmond, CA.

2010 Use of the National YSTR database and YSTR Mixture Deconvolution. Current and Future Advances in Human Identification Conference (hosted by the Virginia Department of Forensic Sciences), Hampton, VA.

2010 Forensic Biology Research at the National Center for Forensic Science. EDNAP (European DNA Profiling Group) Meeting, Kiev, Ukraine

2010 External Visible Trait, Kinship and Ancestry Profiling using Large Scale SNP Panels. European Network of Forensic Science Institutes DNA Working Group Meeting, Kiev, Ukraine

2011 From the Bed to the Bench: Defining the Vaginal and Cervical Environment for Post-Coital DNA Recovery. Speck, P., Faugna, D. and Ballantyne, J. AAFS Annual Meeting, Chicago, IL.

2011 Evolution of DNA Mixture Interpretation. DNA Mixture Interpretation Workshop organized by the National Forensic Science Technology Center, Clearwater Beach, FL.

2011 Interpretation of Y STR Mixtures and Statistical Applications organized by the National Forensic Science Technology Center, Clearwater Beach, FL.

JOURNAL/FUNDING AGENCY REVIEWS

Journal of Forensic Science, Forensic Science International, Biotechniques, Expert Reviews in Molecular Diagnostics, NSERC (Natural Sciences and Engineering Research Council of Canada), Trends in Biotechnology, PLosONE, Department of Justice, National Institute of Justice

PROFESSIONAL ACTIVITIES

1988	Organizer of the Banbury Conference at Cold Spring Harbor Laboratory on DNA Technology and Forensic Science
1991-1998	Member of the NYS DNA User's Group
1992	Chairman/Organizer of the Serology/DNA Session at the Annual Northeastern Association of Forensic Sciences, Atlantic City, NJ
1992-1995	New York State Scientific Review Board
1992	Organizer of the Banbury Conference at Cold Spring Harbor Laboratory, NY on DNA Fingerprinting
1994-1998	Proficiency Review Committee (DNA-PRC) of ASCLD/LAB
1995-1998	ASCLD/LAB Accreditation Inspector
1995-1998	Appointed by the Director of the FBI to the DNA Advisory Board (established by the DNA Identification Act 1994)
1995-2001	Member of FBI's TWGDAM (Technical Working Group on DNA Analysis Methods)
1995-1997	New York State DNA Sub-committee (Chapter 737 of the Laws of 1994)
1996-1998	Participant in the FBI-sponsored STR Standardization project
1996-1998	Appointed by the National Institute of Justice to the National Forensic DNA Review Panel (NFDRP) (established by the DNA Identification Act 1994)
1997-present	Appointed as Chair of New York State DNA Subcommittee (Chapter 737 of the Laws of 1994)
1997	Training Committee Chairperson of NIJ/NIST(OLES)/ASCLD workshop 'Forensic Science Summit: Roadmap to the Year 2000'.
1998-2002	Member of the Credentials Review Committee of ASCLD (established as a result of the issuance by the Director of the FBI of the Quality Assurance Standards for DNA Testing laboratories)
1999-present	Technical Assessor for the Standards Council for Canada
2000-2003	Peer Review Panel Member, National Institute of Justice
2001-2003	Planning panel member, and Member, of NIJ/West Virginia University's TWGED, Technical Working Group on Forensic Science Training and Education

2001-2003	Planning panel member, and Member, of NIJ/NCFS's Technical Working Group on Mass Fatality Incidents (Publication: 'Mass Fatality Incidents: A Guide for Human Forensic Identification')
2001-present	Member of the Department of Defense DNA Quality Assurance Oversight Committee of the Armed Forces Institute of Pathology Scientific Advisory Board, Washington, DC (oversight of the quality assurance program of the Armed Forces DNA Identification Laboratory)
2001-present	Regular 'invited guest' to the FBI's SWGDAM group (Scientific Working Group on DNA Analysis)
2001-2006	Member of the Kinship and DNA Analysis Panel (KADAP). (Set up by NIJ to aid the NYC OCME in the DNA identification efforts in the NYC WTC terrorist incident)
2002-2004	Planning panel member and Member, Florida Emergency Mortuary Operations Response System (system set up by the State of Florida to respond to mass fatalities incidents within the state)
2002-2003	Member of the Scientific Advisory Board, the BODE Technology Group, Springfield, VA
2003-2006	Member of the NIJ/Forensic Resource Network Principles of Forensic DNA for Officers of the Court Technical Working Group
2004	Co-Chair of the Y-STR Analysis on Forensic Casework Workshop, AAFS Annual meeting, Dallas, TX
2004	Moderator, Applied Biosystems Annual User Forum, AAFS Annual Meeting, Dallas, TX
2004	Co-Chair of the Fundamentals of Molecular Biology for Forensic Scientists Workshop. 15th International Symposium on Human Identification, Phoenix, AZ
2005-2006	Member of the Hurricane Victim DNA Identification Expert Group (HVDIEG). (Set up by the State of Louisiana to aid the DNA identification efforts in the hurricane Katrina incident)
2007-present	Member of the NIJ/National Clearing House for Science, Technology and the Law on DNA Evidence for Defense Lawyers Technical Working Group
2007-present	Member of the Editorial Board of the Open Forensic Science Journal (www.bentham.org/open/toforsj).
2008-present	Member of the Editorial Board of the Journal of Forensic Sciences

2008 Organized and taught a workshop 'New Technologies and Applications in Forensic Biology' for the New Jersey State Police, Hamilton, NJ.

2008-present Member of the Advisory Council Committee of the National Clearing House for Science, Technology and the Law at Stetson University College of Law, Gulfport, FL

2008 Organized and taught a workshop 'Y chromosome marker applications in forensic genetics' to the Arizona Department of Public Safety, Phoenix, AZ.

2008 Member of the Scientific Advisory Board of GenVault, Corporation

2010 Member of the Scientific Advisory Board of Identitas Corporation

TEACHING ACTIVITY

STUDENT INSTRUCTION

SUNY, Stony Brook, NY

Seminar in Forensic Biology,	Spring,	1997	HAD 435
Seminar in Forensic Biology,	Spring,	1998	HAD 435

UCF, Orlando, FL

1998-1999

Forensic Serology, Class. Methds	Fall	1998	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	1998	CHS 6535
Lab. Methods for Mol. Biol.	Fall	1998	PCB 6407C
Forensic Serology, Mol. Methds	Spring	1999	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	1999	CHS 6535L
Thesis Research	Spring	1999	CHS 6971

1999-2000

Forensic Serology, Class. Methds	Fall	1999	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	1999	CHS 6535
Thesis Research	Fall	1999	CHS 6971
Forensic Serology, Mol. Methds	Spring	2000	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2000	CHS6535L
Intro. To Forensic Science	Spring	2000	CHS 3501
Thesis Research	Spring	2000	CHS 6971
Introduction to Forensic Science	Summer	2000	CHS 3530
Thesis Research	Summer	2000	CHS 6971

2000-2001

Internship	Fall	2000	CHS 4591

Thesis Research	Fall	2000	CHS 6971
Forensic Biochemistry I	Fall	2000	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2000	CHS 6535
Court Presentation Skills	Fall	2000	CHS 6908
Forensic Biochemistry II	Spring	2001	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2001	CHS6535L
Intro. To Forensic Science	Spring	2001	CHS 3501
Thesis Research	Spring	2001	CHS 6971
Court Presentation Skills	Spring	2001	CHS 6908
Internship	Spring	2001	CHS 4591
Thesis Research	Summer	2001	CHS 6971

2001-2002

Forensic Biochemistry I	Fall	2001	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2001	CHS 6535
Court Presentation Skills	Fall	2001	CHS 6908
Thesis Research	Fall	2001	CHS 6971
Struct. and Funct.of Biomolecules	Fall	2001	IDS 7691
Frontiers in Biomolecular Science	Fall	2001	IDS 7690
Doctoral Research	Fall	2001	IDS7919
Forensic Biochemistry II	Spring	2002	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2002	CHS 6535L
Intro. To Forensic	Spring	2002	CHS 3501
Thesis Research	Spring	2002	CHS 6971
Doctoral Research	Spring	2002	IDS 7919
Thesis Research	Summer	2002	CHS 6971
Doctoral Research	Summer	2002	IDS 7919

2002-2003

Forensic Biochemistry I	Fall	2002	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2002	CHS 6535
Frontiers in Biomolecular Science	Fall	2002	IDS 7690
Thesis Research	Fall	2002	CHS 6971
Dissertation Research	Fall	2002	IDS 7971
Forensic Biochemistry II	Spring	2003	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2003	CHS6535L
Intro. To Forensic Science	Spring	2003	CHS 3501
Thesis Research	Spring	2003	CHS 6971
Dissertation Research	Spring	2003	IDS 7971
Court Presentation Skills	Summer	2003	CHS 6908
Thesis Research	Summer	2003	CHS 6971
Dissertation Research	Summer	2003	IDS 7971

2003-2004

Forensic Biochemistry I	Fall	2003	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2003	CHS 6535

Frontiers in Biomolecular Science	Fall	2003	IDS 7690
Thesis Research	Fall	2003	CHS 6971
Dissertation Research	Fall	2003	IDS 7971
Forensic Biochemistry II	Spring	2004	CHS 4534C
Forensic Analysis of Biol. Mat Lab	Spring	2004	CHS6535L
Intro. To Forensic Science	Spring	2004	CHS 3501
Thesis Research	Spring	2004	CHS 6971
Dissertation Research	Spring	2004	IDS 7971
Court Presentation Skills	Summer	2004	CHS 6908
Thesis Research	Summer	2004	CHS 6971
Dissertation Research	Summer	2004	IDS 7971

2004-2005

Forensic Biochemistry I	Fall	2004	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2004	CHS 6535
Str.Funct.Rel. Biomol. Sci.	Fall	2004	BSC 6432
Thesis Research	Fall	2004	CHS 6971
Dissertation Research	Fall	2004	IDS 7971
Forensic Biochemistry II	Spring	2005	CHS 4534C
Intro. To Forensic Science	Spring	2005	CHS 3501
Thesis Research	Spring	2005	CHS 6971
Dissertation Research	Spring	2005	IDS 7971
Intro. To Forensic Science	Summer	2005	CHS 3501
Thesis Research	Summer	2005	CHS 6971
Dissertation Research	Summer	2005	IDS 7971

2005-2006

Forensic Biochemistry I	Fall	2005	CHS 3533C
Forensic Analysis of Biol. Mat.	Fall	2005	CHS 6535
Str.Funct.Rel. Biomol. Sci.	Fall	2005	BSC 6432
Thesis Research	Fall	2005	CHS 6971
Doctoral Research	Fall	2005	IDS 7919
Graduate Seminar (Court Present.)	Fall	2005	CHS 6908
Directed Research	Fall	2005	CHS 6918
Dissertation	Fall	2005	IDS 7980
Forensic Biochemistry II	Spring	2006	CHS 4534C
Intro. To Forensic Science	Spring	2006	CHS 3501
Forensic Anal Biol Mat Lab	Spring	2006	CHD 6535L
Experimental Molecular Biology	Spring	2006	PCB 4529
Thesis Research	Spring	2006	CHS 6971
Doctoral Research	Spring	2006	IDS 7919
Directed Research	Spring	2006	CHS 6918
Independent Study	Spring	2006	CHS 6908
Directed Research	Spring	2006	CHM 7919
Dissertation	Spring	2006	IDS 7980
Doctoral Research	Summer	2006	IDS 7919

Dissertation	Summer	2006	IDS 7980
Thesis Research	Summer	2006	CHS 6971
Directed Research	Summer	2006	CHS 6918
Directed Research	Summer	2006	CHM 7919

2006-2007

Forensic Biochemistry I	Fall	2006	CHS 3533
Forensic Biochemistry I lab	Fall	2006	CHS 3533L
Str.Funct.Rel. Biomol. Sci.	Fall	2005	BSC 6432
Honors Directed Reading	Fall	2006	CHS 4903H
Directed Research	Fall	2006	CHS 6918
Independent Study	Fall	2006	CHS 6908
Thesis	Fall	2006	CHS 6971
Directed Research	Fall	2006	CHM 7919
Doctoral Research	Fall	2006	IDS 7919
Dissertation	Fall	2006	IDS 7980
Forensic Biochemistry II	Spring	2007	CHS 4534C
Thesis Research	Spring	2007	CHS 6971
Doctoral Research	Spring	2007	IDS 7919
Directed Research	Spring	2007	CHS 6918
Independent Study	Spring	2007	CHS 6908
Directed Research	Spring	2007	CHM 7919
Dissertation	Spring	2007	IDS 7980
Honors Undergrad Research	Spring	2007	CHS 4970
Doctoral Research	Summer	2007	IDS 7919
Dissertation	Summer	2007	IDS 7980
Thesis Research	Summer	2007	CHS 6971
Directed Research	Summer	2007	CHS 6918
Directed Research	Summer	2007	CHM 7919
Honors Undergrad Research	Summer	2007	CHS 4970

2007-2008

Str.Funct.Rel. Biomol. Sci.	Fall	2007	BSC 6432
Forensic Molecular Biology	Fall	2007	CHS 6535
Thesis	Fall	2007	CHS 6971
Directed Research	Fall	2007	CHM 7919
Doctoral Research	Fall	2007	IDS 7919
Dissertation	Fall	2007	IDS 7980
Doctoral Research	Spring	2008	IDS 7919
Dissertation	Spring	2008	IDS 7980
Dissertation	Spring	2008	CHM 7980
Forensic Anal Biol Mat Lab	Spring	2008	CHD 6535L

Thesis	Spring	2008	CHS 6971
Doctoral Research	Summer	2008	IDS 7919
Dissertation	Summer	2008	IDS 7980
Thesis	Summer	2008	CHS 6971
Directed Research	Summer	2008	CHS 6918
Dissertation	Summer	2008	CHM 7980

2008-2009

Forensic Biochemistry I	Fall	2008	CHS 3533
Str.Funct.Rel. Biomol. Sci.	Fall	2008	BSC 6432
Directed Research	Fall	2008	CHM 6918
Dissertation	Fall	2008	CHM 7980
Directed Research	Fall	2008	CHS 6918
Thesis	Fall	2008	CHS 6971
Doctoral Research	Fall	2008	IDS 7919
Dissertation	Fall	2008	IDS 7980
Directed Research	Spring	2009	CHM 6918
Forensic Biochemistry II	Spring	2009	CHS4534C
Doctoral Research	Spring	2009	IDS 7919
Dissertation	Spring	2009	CHM 7980
Directed Research	Spring	2009	CHS 6918
Directed Research	Summer	2009	CHM 6918
Doctoral Research	Summer	2009	IDS 7919
Directed Research	Summer	2009	CHS 6918

2009-2010

Forensic Molecular Biology	Fall	2009	CHS 6535
Str.Funct.Rel. Biomol. Sci.	Fall	2009	BSC 6432
Directed Research	Fall	2009	CHM 6918
Directed Research	Fall	2009	CHS 6918
Dissertation	Fall	2009	IDS 7980
Directed Research	Spring	2010	CHM 6918
Dissertation	Spring	2010	CHM 7980
Forensic Anal Biol Mat Lab	Spring	2010	CHD 6535L
Dissertation	Summer	2010	IDS 7980
Thesis	Summer	2010	CHS 6971
Research	Summer	2010	MCB 4912

2010-2011

Forensic Molecular Biology	Fall	2010	CHS 6535
Forensic Biochemistry I (lecture)	Fall	2010	CHS 3533
Directed Research	Fall	2010	CHM 6918
Thesis	Fall	2010	CHS 6971

Research	Fall	2010	MCB 4912

ADMINISTRATION

1998-2004	Program Coordinator for the Forensic Biochemistry Track within the MS in Industrial Chemistry
2004-present	Program Coordinator for the Forensic Biochemistry Track within the MS in Forensic Science

THESIS/DISSERTATIONS SUPERVISED (Chair/PI)

Graduated:

PhD:
Jane Juusola (PhD, Biomolecular Science, 2005)
Ashley Hall (PhD, Biomolecular Science, 2005)
Michelle Alvarez (PhD, Biomedical Science, 2007)
Erin Hanson (PhD, Biomedical Science, 2008)
April Marrone (PhD, Chemistry, 2009)

MS
Charles Badger (MS, Molecular and Micro-Biology, 2000)
Ashley Hall (MS, Forensic Biochemistry Track, 2001)
Debra Glidewell (MS, Forensic Biochemistry Track, 2001)
George Shiro (MS, Forensic Biochemistry Track, 2001)
Jeffrey Ban (MS, Forensic Biochemistry Track, 2002)
Gigi Raker (MS, Forensic Biochemistry Track, 2003)
Stacey Smith (MS) (MS, Forensic Biochemistry Track, 2003)
Erin Hanson (MS, Forensic Biochemistry Track, 2003)
Darlene Daniels (MS) (MS, Forensic Biochemistry Track, 2003)
Paulina Berdos (MS, Forensic Biochemistry Track, 2004)
Mindy Banton or Setzer (MS, Forensic Biochemistry Track, 2004)
Jeremy Fletcher (MS, Forensic Biochemistry Track, 2004)
Susan Hastings (MS, Forensic Biochemistry Track, 2004)
Christine Sanders (MS, Forensic Biochemistry Track, 2005)
Katherine Press (MS, Forensic Biochemistry Track, 2006)
Pam Smith (MS, Forensic Biochemistry Track, 2006)
Kyle Parker (MS, Forensic Biochemistry Track, 2006)
Micah Halpern (MS, Forensic Biochemistry Track, 2008)

BS
Michelle Josey (BS Honors Thesis, 2007)

Current:

MS:
Christopher Comar (Broward County, FL) (MS, Forensic Biochemistry Track)
Arlene Petrosky (Broward County, FL) (MS, Forensic Biochemistry Track)
Charly Parker (MS, Forensic Biochemistry Track)
Mirianette Gayoso (MS, Forensic Biochemistry Track)

THESIS/DISSERTATION COMMITTEES (not as Chair)

2004-2007 Todd Castoe (PhD, Biomolecular Science)
2001-2004 Oscar Ruiz (PhD, Biomolecular Science)
2002-2004 Claudia Romero (PhD, Biomolecular Science)
2002-2003 Paul Cohill (PhD, Biomolecular Science)
2005-2006 Wang Yiqiang (Danny) (PhD, Chemistry)
2005-2009 Bongyong Lee (PhD, Biomedical Science)
2004-2010 Jose Salvatico (PhD, Biomedical Science)
2008-2010 Minpei Wong (PhD, Biomedical Science)
2008-2009 Sarah Parker (BS Nursing, Honors Thesis)
2010-present Eric Goldstein (Honors in the Major, Molecular Biology)
2010-present Aditya Reddy Kolli (PhD, Chemistry)

EXTERNAL EXAMINER

2005 Curtis Hildebrandt (MS, Lakehead University, Thunder Bay, Canada)
2010 Ursula Zipperer (MS Forensic Science, Virginia Commonwealth University, VA)

PATENTS

2007 Messenger RNA Profiling: Body Fluid Identification Using Multiplex Reverse Transcription-Polymerase Chain Reaction (RT-PCR). Co-inventor with Jane Juusola. United States Patent No: 7,270,983, issued September 18, 2007.

2007 Age Determination from Biological Stains Using Messenger RNA Profiling Analysis. Co-inventor with Michelle Alvarez. United States Patent No: 7,276,340 B1, issued October 2, 2007.

2009 Messenger RNA Profiling: Body Fluid Identification Using Multiplex Reverse Transcription-Polymerase Chain Reaction (RT-PCR). Co-inventor with Jane Juusola. United States Patent No: 7,582,435, issued September 1, 2009.

2009 Messenger RNA Profiling: Body Fluid Identification Using Multiplex Real Time --Polymerase Chain Reaction (Q-PCR). Co-inventor with Jane Juusola. United States Patent No: 7,588,921, issued September 15, 2009.

2010 Age Determination from Biological Stains Using Messenger RNA Profiling Analysis. Co-inventor with Michelle Alvarez. United States Patent No: 7,704,693, issued April 27, 2010.

PUBLICATIONS

A. Peer-Reviewed Journal Articles

1 Chromosomally Integrated Retroviral Substrates are Sensitive Indicators of an Antibody Class Switch Recombinase-Like Activity. Ballantyne, J., Ozsvath, L., Bondarchuk, K. and Marcu, K.B. *Curr. Top. Microbiol. Immunol.* **194**, 439-448 (1995)

2 Forensic Applications of a Rapid, Sensitive and Precise Multiplex Analysis of the Four Short Tandem Repeat Loci HUMVWF31/A., HUMTH01, HUMF13A1, and HUMFES/FPS. Robertson, J.M., Sgueglia, J.B., Badger, C.A., Juston, A.C. and Ballantyne, J. *Electrophoresis* **16**, 1568-1576 (1995)

3 The Applicability of Formalin Fixed and Formalin Fixed Paraffin Embedded Tissues in Forensic DNA Analysis. Romero, R., Juston, A.C., Ballantyne, J. and Henry, B.E. *J. Forensic. Sci.* **42**, 708-714, (1997)

4 Antibody Class Switch Recombinase Activity is B Cell Stage Specific and Functions Stochastically in the Absence of 'Targeted Accessibility' Control. Ballantyne, J., Henry, D. and Marcu, K. *Int. Immunol.* **9**, 963-974, (1997)

5 Mass Disaster Genetics. *Nature Genet.* **15**, 329-331 (1997)

6 Efficient Recombination of a Switch Substrate Retrovector in CD40-Activated B Lymphocytes: Implications for the Control of C_H Gene Switch Recombination. Ballantyne, J., Henry, D.H., Muller, J.R., Briere, F., Snapper, C.M., Kehry, M. and Marcu, K.B. *J. Immunol*., **161**, 1336-1347, (1998)

7 Immunoglobulins: Polyclonal and Monoclonal Antibodies. Ballantyne, J., Mandle, R. and Bing, D.H. Chapter 36 In Hematology: Basic Principles and Practice, Third Edition. Churchill Livingstone, New York, (2000)

8 Messenger RNA Profiling: A Prototype Method to Supplant Conventional Methods for Body Fluid Identification. Juusola, J. and Ballantyne J. *For. Sci. Int.* 135: 85-96 (2003)

9 The Development of an 18 Loci Y-STR system for Forensic Casework. Hall, A. and Ballantyne, J. *Anal Bioanal Chem* 376 1234-1246 (2003)

10 Novel Y-STR Typing Strategies Reveal the Genetic Profile of the Semen Donor in Extended Interval Post Coital Cervicovaginal Samples. Hall, A. and Ballantyne, J. *For Sci Int* 136: 58-72 (2003)

11 Strategies for the Design and Assessment of Y-STR Multiplexes for Forensic Use. Hall, A. and Ballantyne, J. *Forensic Sci Rev* 15(2) 137-149 (2003)

12 The Design and Characterization of a Highly Discriminating 21 Locus Y-STR System for Forensic Casework. Hanson, E. and Ballantyne, J. *J Forensic Sci* 49(1) 1-12 (2004)

13 SWGDAM Developmental Validation of a 19 locus Y-STR System for Forensic Casework. Daniels, D., Hall, A. and Ballantyne, J. *J Forensic Sci* 49 (4) 668-683 (2004)

14 Characterization of UVC-Induced DNA Damage in Physiological Stains: Forensic Implications. Hall, A. and Ballantyne, J. *Anal Bioanal Chem* 380 72-83 (2004)

15 An mRNA and DNA Co-Isolation Method for Forensic Casework Samples. Alvarez, M, Juusola, J and Ballantyne, J. *Anal Biochem* 335: 289-298 (2004)

16 Inference of Human Geographic Origins using *Alu* Insertion Polymorphisms. Ray, D., Walker, J., Hall, A., Llewellyn, B., Ballantyne, J., Christian, A., Turteltaub, K., and Batzer, M. *For Sci Int* 153 117-124 (2005)

17 Multiplex mRNA Profiling for Body Fluid Identification. Juusola, J. and Ballantyne, J. *For Sci Int* 152 1-12 (2005)

18 Whole Genome Amplification Strategy for Forensic Genetic Analysis Using Single or Few Cell Equivalents of Genomic DNA. Hanson, E. and Ballantyne, J. *Anal Biochem* 346 246-257 (2005)

19 DNA Identifications After the 9/11 World Trade Center Attack. Biesecker LG, Bailey-Wilson JE, Ballantyne J, Baum H, Bieber FR, Brenner C, Budowle B, Butler JM, Carmody G, Conneally PM, Duceman B, Eisenberg A, Forman L2, Kidd KK, Leclair B, Niezgoda S, Parsons TJ, Pugh E, Shaler R, Sherry ST, Sozer A, Walsh A. *Science* 310 1122-1123 (2005)

20 Comprehensive Annotated STR Physical Map of the Human Y Chromosome: Forensic Implications. Hanson, E. and Ballantyne, J. *Legal Medicine* (2006) 8 110-120

21 Laser Microdissection Separation of Pure Spermatozoa from Epithelial Cells for STR Analysis. Sanders, C. T., Sanchez, N., Ballantyne, J. and. Peterson, D.A *J. Forensic Sci* 51(4) 748-757 (2006)

22 Novel thermostable Y-family Polymerases: Applications for the PCR Amplification of Damaged or Ancient DNAs. McDonald, J.P., Hall, A., Gasparutto, D., Cadet J., Ballantyne J and Woodgate, R. *Nucleic Acids Res* (2006) 34 (4) 1102-1111

23 The Identification of Newborns Using Messenger RNA Profiling Analysis. Alvarez, M. and Ballantyne, J. *Anal Biochem* 357 21-34 (2006)

24 Testing and Evaluation of 43 'Non-Core' Y Chromosome Markers for Forensic Casework Applications. Hanson, E., Berdos, P. and Ballantyne, J. *J. Forensic Sci* 51(6) 1298-1314 (2006)

25 Y-STR Concordance Study Between Y-Plex™5, Y-Plex™6, Y-Plex™12, Powerplex®, Y-Filer™, MPI, and MPII. Gross, A.M., Berdos, P. and Ballantyne, J. *J. Forensic Sci* 51(6) 1423-28 (2006)

26 Sub-Populations within the Major European and African Derived Haplogroups R1b3 and E3a are Differentiated by Previously Phylogenetically Undefined Y-SNPs. Sims, L.M., Garvey, D. and Ballantyne J. *Human Mut* 28(1) 97 (2007)

27 Population Data for a Novel, Highly Discriminating Tetra-local Y-STR: DYS503. Hanson, E. and Ballantyne, J. *J. Forensic Sci* 52 (2) 498-499 (2007)

28 Simplified Low Copy Number (LCN) DNA Analysis by Post PCR Purification. Smith, P.J. and Ballantyne, J. *J. Forensic Sci* 52 (4) 820-829 (2007)

29 Performance Characteristics of Commercial Y-STR Multiplex Systems. Mayntz-Press, K.A and Ballantyne J. *J. Forensic Sci* 52 (5) 1025-1034 (2007)

30 Population Data for 48 'Non-Core" Y Chromosome Loci. Hanson, E. and Ballantyne, J. *Legal Medicine* 9 221-231 (2007)

31 mRNA Profiling for Body Fluid Identification by Multiplex Quantitative RT-PCR. Juusola, J. and Ballantyne J. *J. Forensic Sci* 52 (6) 1252-1262 (2007)

32 An Ultra-High Discrimination Y Chromosome Short Tandem Repeat Multiplex DNA Typing System. Hanson, E.K. and Ballantyne, J. *PLoS ONE* 2(8): e688. doi:10.1371/journal.pone.0000688 (2007)

33 The *Golden* Gene (SLC24A5) Differentiates US Sub-Populations within the Ethnically Admixed Y-SNP Haplogroups. Sims, L.M. and Ballantyne, J. *Legal Medicine* 10 (2) 72-77 (2008)

34 Recovery and Stability of RNA in Vaginal Swabs and Blood, Semen, and Saliva Stains. Setzer,M., Juusola, J. and Ballantyne, J. *J. Forensic Sci* 53 (2) 296-305 (2008)

35 Y-STR Profiling in Extended Interval (≥ 3 days) Post Coital Cervicovaginal Samples. Mayntz-Press, K.A., Sims, L.M., Hall, A. and Ballantyne J. *J. Forensic Sci* 53 (2) 342-348 (2008)

36 A Rare Y Chromosome Missense Mutation in Exon 25 of Human USP9Y Revealed by Pyrosequencing. Sims, L.M. and Ballantyne, J. *Biochem Genet* 46 154-161 (2008)

37 Sequence Specificity of BAL 31 Nuclease for ssDNA Revealed by Synthetic Oligomer Substrates Containing Homopolymeric Guanine Tracts. Marrone, A. and Ballantyne, J. *PLoS ONE* 3 (10): doi: 10.1371/journal.pone.0003595 (2008)

38 Identification of four novel developmentally regulated gamma hemoglobin mRNA isoforms. Alvarez, M. and Ballantyne, J. *Exp Hematol* 37 285-293 (2009)

39 Identification of Forensically Relevant Body Fluids Using a Panel of Differentially Expressed microRNAs. Hanson, E.K. and Ballantyne, J. *Anal Biochem* 387 303-314 (2009)

40 Changes in Dry State Hemoglobin Over Time Do Not Increase the Potential for Oxidative Damage in Dried Blood. Marrone, A. and Ballantyne,. J. *PLoS ONE* 4(4): e5110. doi:10.1371/journal.pone.0005110 (2009)

41 A comparative analysis of two different sets of Y-chromosome short tandem repeats (Y-STRs) on a common population panel. Maybruck JL, Hanson E, Ballantyne J, Budowle B and Fuerst PA. *Forensic Sci Int Genet* 4 11-20 doi:10.1016/j.fsigen.2009.03.004 (2009)

42 High Resolution Haplogroup G Phylogeny in the Y Chromosome, Revealed by a Set of Newly Characterized SNPs. Sims LM, Garvey D and Ballantyne J. *PLoS ONE* 4(6): e5792. doi:10.1371/journal.pone.0005792 (2009)

43 A SNP melt curve assay employing an intercalating dye probe FRET for forensic analysis. Halpern, MD and Ballantyne J. *Anal Biochem* 391 1-10 (2009)

44 Hydrolysis of DNA and its Molecular Components in the Dry State. Marrone, A. and Ballantyne,. J. *Forensic Sci Int Genet* 4 168-177 (2010)

45 An STR Melt Curve Genotyping Assay for Forensic Analysis Employing an Intercalating Dye Probe FRET. Halpern, MD and Ballantyne, J. *J. Forensic Sci* J Forensic Sci. Sep 14. doi: 10.1111/j.1556-4029.2010.01549.x. (2010) (in press)

46 mRNA Profiling For the Identification of Blood – Results of a Collaborative EDNAP Exercise. Haas C, Hanson E, Bär W, Banemann R, Bento AM, Berti A, Borges E, Bouakaze C, Carracedo A, Carvalho M, Choma A, Dötsch M, Durianciková M, Olsen PH; Hohoff C, Johansen P, Lindenbergh A, Loddenkötter B, Ludes B, Maroñas O, Morling N, Niederstätter H, Parson W, Sijen T, Sviezená B, Zatkalíková L and Ballantyne J. *Forensic Sci Int Genet* 5 21-26 (2011)

47 RNA Profiling for the Identification of the Tissue Origin of Dried Stains in Forensic Biology**.** Hanson, EK and Ballantyne, J. *Forensic Sci Rev* 22 (2) 145-157 (2010)

48 A Single Molecular Beacon is Sufficient for the Analysis of Multiple Nucleaic Acid Sequences. Gerasimova, Y, Hayson, A, Ballantyne, J and Kolpashchikov, D. *ChemBioChem* 11 1762-1768 (2010)

49 A Blue Spectral Shift of the Hemoglobin Soret Band Correlates with the Age (Time since Deposition) of Dried Bloodstains. Hanson, EK and Ballantyne, J. *PLoSONE* 5(9):e12830. doi:10.1371/journal.pone.0012830 (2010)

50 US Forensic Y Chromosome Short Tandem Repeats Database. Ge, J., Budowle, B., Planz, J.V., Eisenberg, A.J., Ballantyne, J. and Chakraborty, R. *Legal Medicine* 12 289-295 (2010)

51 Selection of Highly Specific and Sensitive mRNA Biomarkers for the Identification of Blood. Haas, C., Hanson, E., Kratzer, A., Bar, W. and Ballantyne, J. *Forensic Sci Int Genet* doi: 10.1016/j.fsigen.2010.09.006 (2010)(in press)

52 RNA/DNA Co-analysis from Bloodstains – Results of a Second Collaborative EDNAP Exercise. Haas C, Hanson E, Anjos MJ, Bär W, Banemann R, Berti A, Borges E, Bouakaze C, Carracedo A, Carvalho M, Castella V, Choma A, De Cock G, Dötsch M, Hoff-Olsen P, Johansen P, Kohlmeier F, Lindenbergh A, Ludes B, Maroñas O, Moore D, Morerod M-L, Morling N, Niederstätter H, Noel F, Parson W, Patel G, Popielarz C, Salata E, Schneider PM, Sijen T, Sviezená B, Turanska M, Zatkalikova L and Ballantyne J. *Forensic Sci Int Genet* doi:10.1016/j.fsigen.2011.02.004 (2011) (in press)

B. Books and Monographs

1 DNA Technology in a County Forensic Science Laboratory Setting. In Banbury Conference on 'DNA Technology and Forensic Science.' Cold Spring Harbor Laboratory Press, NY. (1989)

2 Banbury Report 32: DNA Technology and Forensic Science. Ed. Ballantyne, J., Sensabaugh, G. and Witkowski, J. New York: Cold Spring Harbor Laboratory Press, NY. (1989)

3 Serology Overview. Ballantyne J. In Encyclopedia of Forensic Science, Academic Press, London (2000)

4 Serology Overview. Ballantyne J. In *Encyclopedia of Forensic and Legal Medicine*, Elsevier, Oxford. Payne James, J., Byard, R., Corey, T and Henderson, C (Eds). (2005) ISBN: 0-12-547970

5 Creating and Managing Effective Y-STR Databases. Ballantyne, J., Fatolitis, L. and Roewer. *Profiles in DNA* 9(2) 10-13 (2006)

6 Validity of Messenger RNA Expression Analyses of Human Saliva. Ballantyne J. Letter to Editor. *Clin Cancer Res* 13 (4) 1350 (2007)

7 The US Y-STR Database. Fatolitis, L. and Ballantyne, J. *Profiles in DNA* 11(1) 13-14 (2008)

8 Review of: *Molecular Photofitting*. Ballantyne J. Book Review. *J Forensic Sci* 53 (4) 1010 (2008)

9 The Uses of Saliva in Forensic Genetics. Ballantyne,J. and Juusola, J. In *Salivary Diagnostics*, Wiley-Blackwell, Ames, Iowa, USA. Wong, DT (Ed). (2008) ISBN: 978-0-8138-1333-2.

10 Preparation of Forensic Samples for Direct Molecular Applications. Hanson, E.K. and Ballantyne, J. In *Handbook of Nucleic Acid Purification*, CRC Press, Boca Raton, FL, USA. Liu, D. (Ed). (2009) ISBN: 978-1-4200-7096-5.

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FUNDED PROJECTS
Summary: Since May 2001, 40 awards totaling $6.48 million.

EXPERT TESTIMONY
Testified as an expert witness in Courts of Law in US, Scotland, England and Hong Kong

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